

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 07:36:12 ; Search time 63 Seconds

(without alignments)
8202.386 Million cell updates/sec

Title: US-09-854-562-1

Perfect score: 1685

Sequence: 1 CTTAAACATTATTATTC.....TTCAAAAAAAAAAAAA 1685

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 segs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
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5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/Backfillsl.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1685	100.0	1685	1	US-08-362-512A-1
2	1685	100.0	1685	4	US-08-964-939-1
3	507.8	30.1	1740	1	US-08-362-512A-3
4	507.8	30.1	1740	4	US-08-964-939-3
5	53.2	3.2	1682	4	US-09-370-253-1
6	51.6	3.1	1016	4	US-09-370-253-3
7	47.6	2.8	1685	4	US-09-370-253-5
8	46	2.7	1703	4	US-09-370-253-9
9	37.2	2.2	7218	1	US-08-332-463-14
10	36.2	2.1	1960	4	US-09-513-057C-12
11	36.2	2.1	3617	4	US-09-513-057C-14
12	35.4	2.1	7218	4	US-09-149-476-65
13	35.4	2.1	7218	4	US-08-232-463-14
14	35.2	2.1	1863	4	US-09-637-118B-1
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16	35	2.1	2518	4	US-09-513-057C-1
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18	35	2.1	4221	4	US-09-513-057C-3
19	35	2.1	4221	4	US-09-513-057C-34
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21	34.4	2.0	756	3	US-08-822-322-7
22	34.4	2.0	756	4	US-09-466-109-7
23	34.4	2.0	1001	4	US-09-641-638-89
24	34.2	2.0	915	4	US-09-149-476-157
25	34.2	2.0	915	4	US-09-149-476-294
26	34	2.0	1533	4	US-09-134-001C-531
27	34	2.0	2332	1	US-08-618-164-1

28	34	2.0	2649	2	US-08-718-964-1	Sequence 1, Appl
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30	34	2.0	2649	2	US-08-842-341-1	Sequence 1, Appl
31	34	2.0	5703	4	US-09-280-590A-36	Sequence 36, Appl
32	33.4	2.0	390	4	US-09-134-001C-2354	Sequence 2354, Ap
33	33.4	2.0	405	4	US-09-134-001C-2395	Sequence 2395, Ap
34	33.4	2.0	1732	1	US-08-417-330A-17	Sequence 17, Appl
35	33.2	2.0	731	4	US-09-641-638-87	Sequence 87, Appl
36	33.2	2.0	788	4	US-09-641-638-88	Sequence 88, Appl
37	32.8	1.9	616	2	US-08-630-822A-93	Sequence 93, Appl
38	32.8	1.9	616	2	US-09-005-069-93	Sequence 93, Appl
39	32.8	1.9	616	4	US-09-171-156A-42	Sequence 42, Appl
40	32.8	1.9	1065	4	US-08-765-907A-7	Sequence 7, Appl
41	32.8	1.9	1080	4	US-09-668-680-9	Sequence 9, Appl
42	32.8	1.9	2619	4	US-08-983-502-17	Sequence 17, Appl
43	32.8	1.9	2619	5	PCT-US96-10521-17	Sequence 17, Appl
44	32.8	1.9	2887	4	US-08-983-502-14	Sequence 14, Appl
45	32.8	1.9	2887	5	PCT-US96-10521-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-362-512A-1
; Sequence 1, Application US/08362512A
; Patent No. 5719043
; GENERAL INFORMATION:
; APPLICANT: FROMMER, Wolf-Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR AN AMINO ACID
; TITLE OF INVENTION: TRANSPORTER, PLASMIDS, BACTERIA, YEASTS AND PLANTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,512A
; FILING DATE: 05-JAN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/007,636
; FILING DATE: 21-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meliman, Edward A.
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: P/951-107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 382-0700
; TELEFAX: (212) 382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 57..1511
; OTHER INFORMATION: /note= "amino acid transporter"

QY 1681 AAAAA 1685
DB 1681 AAAAA 1685

RESULT 3

US-08-362-512A-3
; Sequence 3, Application US/08362512A

; Patent No. 5719043

; GENERAL INFORMATION:

; APPLICANT: FROMMER, Wolf-Bernd

; TITLE OF INVENTION: DNA SEQUENCES FOR AN AMINO ACID

; TITLE OF INVENTION: TRANSPORTER, PLASMIDS, BACTERIA, YEASTS AND PLANTS

; TITLE OF INVENTION: CONTAINING A TRANSPORTER AND THEIR USE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen

; STREET: 1180 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: US

; ZIP: 10036-8403

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/362.512A

; FILING DATE: 05-JAN-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/007,636

; FILING DATE: 21-JAN-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Meilman, Edward A.

; REGISTRATION NUMBER: 24,735

; REFERENCE/DOCKET NUMBER: P/951-107

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 382-0700

; TELEFAX: (212) 382-0888

; TELEX: 236925

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1740 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 80..1558

; OTHER INFORMATION: /product= "amino acid transporter"

US-08-362-512A-3

Query Match 30.1%; Score 507.8; DB 1; Length 1740;

Best Local Similarity 59.2%; Pred. No. 7.8e-154;

Matches 921; Conservative 0; Mismatches 627; Indels 7; Gaps 3;

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DB 185 AAATGCTTCGATGATGATGGCCGCTCAAAAGAACTGGGACTGTTTGGACCGGAGCGCT 244

QY 195 CATATTATCAGCGGTGATAGCTCCGAGTGTGTCTTTAGCATGGGCTATAGCTCAG 254

DB 245 CATATAAATACATGCGGTATCGATCCGCGGTTTGTCAITGGGTGGCGGATTCACAG 304

QY 255 CTTGGTTGATCGCAGGACATCGATCTTACTCATTTTCGTTTCAATTACTTACTTCCAC 314

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QY 315 TCCACCATGCTTTGCCGATTGCTACGTCGCCGATCCGTCACCGAAAAACGGAATTAC 374
DB 365 TCCACCATGCTTTAGGACTGCTACAGAACCGCGGATGAGTGTCTGGCAAGAGAACTAC 424
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DB 425 ACTTACATGGATGCGGTTTCGATCAATTCTCGTGGTTCAGATTCAAGATTGTGGGTTG 484
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QY 495 TTGGTAGCGGTAGGAAATCGAACTGTTCCACGATAAGGCGCACACGCGGATTTGTTACT 554
DB 545 ATGATGGCGATCAAGAGATCAACTGCTTCCAAAGATGGAGGAAAGACCCATGTCTAC 604
QY 555 ATATCGAATTATCCGATATATATGGCGGTTTTTGGTATCATTTCAAGTTATTCTTAGCCAGATC 614
DB 605 ATGTCAGTAATCTTTACATGATCGTATTGTTGGTCAGAGATCTTGTCTCTCAGGTT 664
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DB 725 TCTGCCATTTGGTCTAGCTCTTTGGAATCGTCAAGTTGGAGCAATGGAGTTTTCAAAGA 784
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DB 842 TTCCAAGCACTTGGAGACATTTGCCCTTTTCGCTACTCATCTCTGTTGCTTAATCGAGATT 901
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DB 962 AGTATGCGGTCACAACCTATCTTCTACATGCTATGTGGCTCAATGGGTTATGCCGCTTT 1021
QY 975 GGAACAATGCCCTGGAGATTTCTCTACAGATTTCGGGTTTTTCGAGCCCTTTTGGGCTC 1034
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QY 1095 CAGCGGATATTCAGTTTGTGAGAAAAAATGCAACAGAAACTATCCAGACAAACAGTTC 1154
DB 1142 CAGCCCATCTTTGCTTTTATTTGAAAAAATCAGTCGAGAGAGATATCCAGACAACTCTC 1201
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Qy	1392	ATTCGCGCTGAAAAAGATGCTCTATGTTGCTGATGATGCTGCTCTTGACGACCGGA	1451
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1 RESULT 4
2 US-08-964-939-3
3 ; Sequence 3, Application US/08964939
4 ; Patent No. 6243970
5 ;
6 ; GENERAL INFORMATION:
7 ; APPLICANT: FROMMER, Wolf-Bernd
8 ; TITLE OF INVENTION: DNA SEQUENCES FOR AN AMINO ACID
9 ; TITLE OF INVENTION: TRANSPORTER, PLASMIDS, BACTERIA, YEASTS AND PLANTS
10 ; TITLE OF INVENTION: CONTAINING A TRANSPORTER AND THEIR USE
11 ; NUMBER OF SEQUENCES: 4
12 ;
13 ; CORRESPONDENCE ADDRESS:
14 ; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
15 ; STREET: 1180 Avenue of the Americas
16 ; CITY: New York
17 ; STATE: NY
18 ;
19 ; COUNTRY: US
20 ; ZIP: 10036-8403
21 ;
22 ; COMPUTER READABLE FORM:
23 ; MEDIUM TYPE: Floppy disk
24 ; COMPUTER: IBM PC compatible
25 ; OPERATING SYSTEM: PC-DOS/MS-DOS
26 ; SOFTWARE: Patentin Release #1.0, Version #1.25
27 ;
28 ; CURRENT APPLICATION DATA:
29 ; APPLICATION NUMBER: US/08/964,939
30 ; FILING DATE:
31 ;
32 ; CLASSIFICATION: 800
33 ; PRIOR APPLICATION DATA:
34 ; APPLICATION NUMBER: US 08/362,512
35 ; FILING DATE: 05-JAN-1995
36 ; APPLICATION NUMBER: US 08/007,636
37 ; FILING DATE: 21-JAN-1993
38 ;
39 ; ATTORNEY/AGENT INFORMATION:
40 ; NAME: Meliman, Edward A.
41 ; REGISTRATION NUMBER: 24,735
42 ;
43 ; REFERENCE/DOCKET NUMBER: P/951-107
44 ;
45 ; TELECOMMUNICATION INFORMATION:
46 ; TELEPHONE: (212) 382-0700
47 ; TELEFAX: (212) 382-0888
48 ;
49 ; TELEX: 236925
50 ;
51 ; INFORMATION FOR SEQ ID NO: 3:
52 ;
53 ; SEQUENCE CHARACTERISTICS:
54 ; LENGTH: 1740 base pairs
55 ; TYPE: nucleic acid
56 ; STRANDEDNESS: single
57 ; TOPOLOGY: linear
58 ;
59 ; MOLECULE TYPE: cDNA
60 ;
61 ; ORIGINAL SOURCE:
62 ; ORGANISM: Arabidopsis thaliana
63 ;
64 ; FEATURE:
65 ; NAME/KEY: CDS
66 ; LOCATION: 80..1558
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68 ; OTHER INFORMATION: /product= "amino acid transporter"
69 ;

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	Query Match	Score	DB #	Length
	Best Local Similarity	59.2%;	Pred. No. 7.8e-15;	
Matches	921; Conservative	0;	Mismatches 62;	Indels 7; Gaps 3

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Qy	495	TTGTAGCGGTAGGGAAATGAACTGCTCTTCCACGATTAAGGSCACACTGCGGATTTACT	554
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Db	902	CAGATACCTGTAGATCTCCACCGCGGGAGATGAAACATATGAAGAACCAAAATTC	961
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RESULT 5

US-09-370-253-1

; Sequence 1, Application US/09370253

; Patent No. 6165792

; GENERAL INFORMATION:

; APPLICANT: Allen, Stephen M.

; APPLICANT: Sakai, Hajime

; APPLICANT: Thorpe, Catherine J.

; TITLE OF INVENTION: Amino Acid Transporters

; FILE REFERENCE: BB-1200

; CURRENT APPLICATION NUMBER: US/09/370,253

; CURRENT FILING DATE: 1999-08-09

; EARLIER APPLICATION NUMBER: 60/097,222

; EARLIER FILING DATE: August 20, 1998

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 1

; LENGTH: 1882

; TYPE: DNA

; ORGANISM: Hordeum vulgare

US-09-370-253-1

Query Match 3.2%; Score 53.2; DB 4; Length 1882;

Best Local Similarity 51.1%; Pred. No. 9.5e-07;

Matches 183; Conservative 0; Mismatches 163; Indels 12; Gaps 2;

QY 768 ACCGAGCTCAAAAGATATGGAGATCGTTTCAAGCGGTTTGGGACATACGTTTCGCTAT 827
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QY 828 GCTTATGCCACGGTTCTTATCGAGATTCAGGATACACTAAGATCTAGCCAG-----CT 881
DB 790 TCCGGCCAAATGTGGTGTAGAAATTCAGGCTTACCATCCATCGACGCCCGCAACCG 849
QY 882 GAGAACAAAGCCATGAAAGAGCAAGTCTTGTGGGAGTATCAACCACCACCTTTTCTAC 941

DB 850 TCCAAAGACCAATGTGAAGGCGTGTGTGCGCTACATCATCGCCCTGCTAC 909
QY 942 ATCTTATGTGATGATCGGCTATGCTGCATTTGGAAACAATGCCCCCTGGAGATTTCTC 1001
DB 910 TTCCCGGTGGCAATTTATCGGTACTGCGCATTTTGGCAACAGCGTCGACGACAATCCTC 969
QY 1002 ACAGATTTTCGGGTTTTCGAGCCCTTTTGGCTCATTTGACTTTTGCAGAGGCTTGCATCGCT 1061
DB 970 A-----TCACCCCTCAACAGCCCAAGTGGCTCATCGCCATGGCCAAACATGATGGTCTC 1023
QY 1062 GTCCACCTTATTTGGTGCCTATCAGGTGTTCCGCGAGCGGATATTTCCAGTTTGTGAGA 1119
DB 1024 GTTCACTCATCGGTAGCTACAGATTTATCGGATGCGGTTGTTGACATGATGAGA 1081

RESULT 6

US-09-370-253-3

; Sequence 3, Application US/09370253

; Patent No. 6165792

; GENERAL INFORMATION:

; APPLICANT: Allen, Stephen M.

; APPLICANT: Sakai, Hajime

; APPLICANT: Thorpe, Catherine J.

; TITLE OF INVENTION: Amino Acid Transporters

; FILE REFERENCE: BB-1200

; CURRENT APPLICATION NUMBER: US/09/370,253

; CURRENT FILING DATE: 1999-08-09

; EARLIER APPLICATION NUMBER: 60/097,222

; EARLIER FILING DATE: August 20, 1998

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 3

; LENGTH: 1016

; TYPE: DNA

; ORGANISM: Zea mays

US-09-370-253-3

Query Match 3.1%; Score 51.6; DB 4; Length 1016;

Best Local Similarity 50.8%; Pred. No. 2.1e-06;

Matches 182; Conservative 0; Mismatches 164; Indels 12; Gaps 2;

QY 768 ACCGAGCTCAAAAGATATGGAGATCGTTTCAAGCGGTTTGGGACATAGCGTTTCGCTAT 827
DB 98 ACCAGCGGGGAAGGTGTTCCGGCTTCTTCGGCGCGCTGGGGGAGCTGGCGCTTCGCTAC 157
QY 828 GCTTATGCCACGGTTCTCATCGAGATTCAGGATACACTAAGATCTAGCCACAGCTGAG--- 884
DB 158 GCGGCCACACAGTGGTGTGAGATCCAGGCCACCATCCCGTCCACCCCGACACGCG 217
QY 885 ---AACAAAGCCATGAAAGAGCAAGTCTTGTGGAGTATCAACACCACTTTTTCCTAC 941
DB 218 TCCAAGAGGCCCATGTGGAAGGCGTGTGTGCTCGCTACGTCGTGGCGCTCTGCTAC 277
QY 942 ATCTATGTGATGCATCGGCTATGCTGCATTTGGAACAATGCCCTCGGAGATTTCTCCTC 1001
DB 278 TTCCCGCTCGGCTCATCGGCTACTGGGCGTTTCGGAACACCGTTCGAGGACAACATCCTC 337
QY 1002 ACAGATTTTCGGGTTTTCGAGCCCTTTTGGCTCATTTGACTTTTGCAGAGGCTTGCATCGCT 1061
DB 338 A-----TCACGCTCAGCAAGCCCAAGTGGCTCATCGGCTCGCCACATGATGGTCTC 391
QY 1062 GTCCACCTTATTTGGTGCCTATCAGGTGTTCCGCGAGCGGATATTTCCAGTTTGTGAGA 1119
DB 392 GTCCATGTCTCGGCGAGCTACAGATCTATGCCATGCGGTTTGTGACATGATGAGA 449

RESULT 7

US-09-370-253-5

; Sequence 5, Application US/09370253

; Patent No. 6165792

; GENERAL INFORMATION:

; APPLICANT: Allen, Stephen M.

APPLICANT: Sakai, Hajime
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: Amino Acid Transporters
FILE REFERENCE: BB-1200
CURRENT APPLICATION NUMBER: US/09/370,253
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: 60/097,222
EARLIER FILING DATE: August 20, 1998
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Microsoft Office 97
SEO ID NO 5
LENGTH: 1865
TYPE: DNA
ORGANISM: Oryza sativa
US-09-370-253-5

Query Match 2.8%; Score 47.6; DB 4; Length 1865;
Best Local Similarity 50.6%; Pred. No. 6.1e-05;
Matches 175; Conservative 0; Mismatches 159; Indels 12; Gaps 2;

QY 780 AAGATATGAGATCGTTTCAAGCGTTGGGACATAGCCGTTCCCTATGCTTATGCGCAG 839
DB 784 AAGGTGTGGCTCTTCTTCACGGCGCTGGGACGTCGCTTCCGCTACGCGGGGACAC 843
QY 840 GTTCTCATCGAGATTGAGATACATAAGATCTAGCCGACCTGAG-----AACAAAGCC 893
DB 844 GTGCTGTGAGATTCAGGAGGACATCCGTCGACCGCGGAGAAAGCCGTCAGAAAGCCG 903
QY 894 ATGAAAAGACAGTCTTGTGGAGATACACCACTTTTTCATCTTATGTGGA 953
DB 904 ATGTGAGAGGCGTCGTCGCGCTCATCATCATGTCGCGCTGCTACCTTCCCGTGGCG 963
QY 954 TGCATGCGCTATGCTGATTTGGAACAATGCCCTGAGATTTCCTCAGATTTGGG 1013
DB 964 CTGTGCGATACGCGGCTTCGACACGATGACACCAATCTCA-----TCAGC 1017
QY 1014 TTTTTCAGCGCTTTGGCTCATTTGCAACTTTCGAACGCTGCACTGCTCACTTATT 1073
DB 1018 CTCTCCAGGCGCAATGCGCTCATCGGCTGCAAAACATGATGGCGCTCATGTCATC 1077
QY 1074 GGTGCTATCAGGTGTTGCGGACCGGATATTCAGTTTGTGGA 1119
DB 1078 GGGAGCTACCAAGATCTACGCGCATGCCGTGTGACATGATGAGA 1123

RESULT 8
US-09-370-253-9

Sequence 9, Application US/09370253
Patent No. 6165792
GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Sakai, Hajime
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: Amino Acid Transporters
FILE REFERENCE: BB-1200
CURRENT APPLICATION NUMBER: US/09/370,253
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: 60/097,222
EARLIER FILING DATE: August 20, 1998
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Microsoft Office 97
SEO ID NO 9
LENGTH: 1703
TYPE: DNA
ORGANISM: Triticum aestivum
US-09-370-253-9

Query Match 2.7%; Score 46; DB 4; Length 1703;
Best Local Similarity 50.3%; Pred. No. 0.00019;
Matches 174; Conservative 0; Mismatches 160; Indels 12; Gaps 2;
QY 780 AAGATATGAGATCGTTTCAAGCGTTGGGACATAGCCGTTCCCTATGCTTATGCGCAG 839

DB 737 AAGGTGTGGCTCTTTCGCGGCGCTGGGCGAAGTGGCTTGCCTGATCCCGGCCAAC 796
QY 840 GTTCTCATCGAGATTGAGATACATAAGATCTAGCCGACCTGAG-----AACAAAGCC 893
DB 797 GTGTGCTGAGATTCAGGAGGACCATCCGTCACGCGCGGAGAAAGCCGTCAGAAAGCC 856
QY 894 ATGAAAAGACAGTCTTGTGGAGATACACCACTTTTTCATCTTATGTGGA 953
DB 857 ATGTGAGAGGCGTGTGTGGCTCATCATGTCGCTGCTGCTACCTTCCCGTGGCGC 916
QY 954 TGCATGCGCTATGCTGATTTGGAACAATGCCCTGAGATTTCCTCAGATTTGGG 1013
DB 917 CTGATGCGCTACTGGGCTTTCGCAACAGCGTCGACGACACATCTCA-----TCACC 970
QY 1014 TTTTTCAGCGCTTTGGGCTCATTTGCAACTTTCGAACGCTTGCATGCTGCTCACTTATT 1073
DB 971 CTCACAAAGCCGCTGCTCATCTCCACCGCCACATATGTTTTCATCTATGTCATC 1030
QY 1074 GGTGCTATCAGGTGTTGCGGACCGGATATTCAGTTTGTGGA 1119
DB 1031 GGAAGCTACCAAGATTACGCGATGCCGTGTGACATGATGAGA 1076

RESULT 9
US-08-232-463-14

Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:

APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: EP 91 114 300.6
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-Fls
US-08-232-463-14

Query Match 2.2%; Score 37.2; DB 1; Length 7218;

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; Sequence 14, Application US/09513057C
; Patent No. 6433251
; GENERAL INFORMATION:
; APPLICANT: Wagner, et al.
; TITLE OF INVENTION: GENES REGULATING CIRCADIAN CLOCK FUNCTION AND PHOTOPERIODISM
; FILE REFERENCE: 1505-54357
; CURRENT APPLICATION NUMBER: US/09/513,057C
; CURRENT FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 3617
; TYPE: DNA
; ORGANISM: Cardamine oligosperma
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(306)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (307)..(531)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (819)..(1531)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (2510)..(2561)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (2646)..(3615)
; OTHER INFORMATION: partial
; NAME/KEY: Intron
; LOCATION: (532)..(818)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (1532)..(2509)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (2562)..(2645)
; OTHER INFORMATION:
; NAME/KEY: unsure
; LOCATION: (1412)..(1412)
; OTHER INFORMATION: W = a or t/u
; NAME/KEY: unsure
; LOCATION: (1409)..(1412)
; OTHER INFORMATION: encoded amino acid is unsure due to nucleotide uncertainty
; NAME/KEY: unsure
; LOCATION: (1406)..(1406)
; OTHER INFORMATION: K = g or t/u
; NAME/KEY: unsure
; LOCATION: (1404)..(1406)
; OTHER INFORMATION: encoded amino acid is unsure due to nucleotide uncertainty
; NAME/KEY: unsure
; LOCATION: (1419)..(1419)
; OTHER INFORMATION: R = a or c
; NAME/KEY: unsure
; LOCATION: (1419)..(1421)
; OTHER INFORMATION: encoded amino acid is unsure due to nucleotide uncertainty
; US-09-513-057C-14
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Query Match 2.1%; Score 36.2; DB 4; Length 1960;
Best Local Similarity 56.2%; Pred. No. 0.31; Mismatches 53; Indels 0; Gaps 0;
Matches 68; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1068 CTTATTGGTGCCTATCAGGTGTTCCGCGAGCGGATATCCAGTTGTTGAGAAAAATGC 1127
Db 1000 CTTATTGGTGCATCACCAGGATATCGTGCTCGAGCAATCAATTACCTTGGAAGATTCT 1059
QY 1128 AACAGAACTATCCAGACAAAGTTTCATCTCTGAAATATTCAGTAAACGTAACCTTTC 1187
Db 1060 GCTAAAGCTATCCAGTGAAGAAGCTCGTTCATCAGAAATTTATCGTAAAGCTCTCTTA 1119
QY 1188 C 1188
Db 1120 C 1120

RESULT 11
US-09-513-057C-14
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```
; Sequence 12, Application US/09513057C
; Patent No. 6433251
; GENERAL INFORMATION:
; APPLICANT: Wagner, et al.
; TITLE OF INVENTION: GENES REGULATING CIRCADIAN CLOCK FUNCTION AND PHOTOPERIODISM
; FILE REFERENCE: 1505-54357
; CURRENT APPLICATION NUMBER: US/09/513,057C
; CURRENT FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1960
; TYPE: DNA
; ORGANISM: Cardamine oligosperma
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1959)
; OTHER INFORMATION:
; US-09-513-057C-12
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; Sequence 14, Application US/09513057C
; Patent No. 6433251
; GENERAL INFORMATION:
; APPLICANT: Wagner, et al.
; TITLE OF INVENTION: GENES REGULATING CIRCADIAN CLOCK FUNCTION AND PHOTOPERIODISM
; FILE REFERENCE: 1505-54357
; CURRENT APPLICATION NUMBER: US/09/513,057C
; CURRENT FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 3617
; TYPE: DNA
; ORGANISM: Cardamine oligosperma
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(306)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (307)..(531)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (819)..(1531)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (2510)..(2561)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (2646)..(3615)
; OTHER INFORMATION: partial
; NAME/KEY: Intron
; LOCATION: (532)..(818)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (1532)..(2509)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (2562)..(2645)
; OTHER INFORMATION:
; NAME/KEY: unsure
; LOCATION: (1412)..(1412)
; OTHER INFORMATION: W = a or t/u
; NAME/KEY: unsure
; LOCATION: (1409)..(1412)
; OTHER INFORMATION: encoded amino acid is unsure due to nucleotide uncertainty
; NAME/KEY: unsure
; LOCATION: (1406)..(1406)
; OTHER INFORMATION: K = g or t/u
; NAME/KEY: unsure
; LOCATION: (1404)..(1406)
; OTHER INFORMATION: encoded amino acid is unsure due to nucleotide uncertainty
; NAME/KEY: unsure
; LOCATION: (1419)..(1419)
; OTHER INFORMATION: R = a or c
; NAME/KEY: unsure
; LOCATION: (1419)..(1421)
; OTHER INFORMATION: encoded amino acid is unsure due to nucleotide uncertainty
; US-09-513-057C-14
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Query Match 2.1%; Score 36.2; DB 4; Length 3617;
Best Local Similarity 56.2%; Pred. No. 0.46; Mismatches 53; Indels 0; Gaps 0;
Matches 68; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1068 CTTATTGGTGCCTATCAGGTGTTCCGCGAGCGGATATCCAGTTGTTGAGAAAAATGC 1127
Db 2655 CTTATTGGTGCATCACCAGGATATCGTGCTCGAGCAATCAATTACCTTGGAAGATTCT 2714
QY 1128 AACAGAACTATCCAGACAAAGTTTCATCTCTGAAATATTCAGTAAACGTAACCTTTC 1187
Db 2715 GCTAAAGCTATCCAGTGAAGAAGCTCGTTCATCAGAAATTTATCGTAAAGCTCTCTTA 2774
QY 1188 C 1188
```


Db 2775 C 2775

RESULT 12

US-09-149-476-65
Sequence 65, Application US/09149476

Patent No. 6420526

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 186 Human Secreted proteins

FILE REFERENCE: P2002P1

CURRENT APPLICATION NUMBER: US/09/149,476

EARLIER FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: PCT/US98/04493

EARLIER FILING DATE: 1998-03-06

EARLIER APPLICATION NUMBER: 60/040,162

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,333

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/038,621

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,626

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,334

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,336

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,163

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/047,600

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,615

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,597

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,502

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,633

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,583

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,617

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,618

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,503

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,592

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,581

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,584

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,500

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,587

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,492

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,598

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,613

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,582

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,596

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,612

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,632

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,601

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/043,580

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,568

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,314

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,569

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,311

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,671

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,674

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,669

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,312

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,313

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,672

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,315

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/048,974

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/056,886

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,877

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,889

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,893

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,662

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,630

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,878

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,882

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,888

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,637

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,903

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,888

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,879

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,880

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,894

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,911

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,636

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,874

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,910

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,864

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,631

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,845

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,892

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/057,761

1	EARLIER FILING DATE: 1997-08-22	
2	EARLIER APPLICATION NUMBER: 60/047,595	
3	EARLIER FILING DATE: 1997-05-23	
4	EARLIER APPLICATION NUMBER: 60/047,599	
5	EARLIER FILING DATE: 1997-05-23	
6	EARLIER APPLICATION NUMBER: 60/047,588	
7	EARLIER FILING DATE: 1997-05-23	
8	EARLIER APPLICATION NUMBER: 60/047,585	
9	EARLIER FILING DATE: 1997-05-23	
10	EARLIER APPLICATION NUMBER: 60/047,586	
11	EARLIER FILING DATE: 1997-05-23	
12	EARLIER APPLICATION NUMBER: 60/047,590	
13	EARLIER FILING DATE: 1997-05-23	
14	EARLIER APPLICATION NUMBER: 60/047,594	
15	EARLIER FILING DATE: 1997-05-23	
16	EARLIER APPLICATION NUMBER: 60/047,589	
17	EARLIER FILING DATE: 1997-05-23	
18	EARLIER APPLICATION NUMBER: 60/047,593	
19	EARLIER FILING DATE: 1997-05-23	
20	EARLIER APPLICATION NUMBER: 60/047,614	
21	EARLIER FILING DATE: 1997-05-23	
22	EARLIER APPLICATION NUMBER: 60/043,578	
23	EARLIER FILING DATE: 1997-04-11	
24	EARLIER APPLICATION NUMBER: 60/043,576	
25	EARLIER FILING DATE: 1997-04-11	
26	EARLIER APPLICATION NUMBER: 60/047,501	
27	EARLIER FILING DATE: 1997-05-23	
28	EARLIER APPLICATION NUMBER: 60/043,670	
29	EARLIER FILING DATE: 1997-04-11	
30	EARLIER APPLICATION NUMBER: 60/056,632	
31	EARLIER FILING DATE: 1997-08-22	
32	EARLIER APPLICATION NUMBER: 60/056,664	
33	EARLIER FILING DATE: 1997-08-22	
34	EARLIER APPLICATION NUMBER: 60/056,876	
35	EARLIER FILING DATE: 1997-08-22	
36	EARLIER APPLICATION NUMBER: 60/056,881	
37	EARLIER FILING DATE: 1997-08-22	
38	EARLIER APPLICATION NUMBER: 60/056,909	
39	EARLIER FILING DATE: 1997-08-22	
40	EARLIER APPLICATION NUMBER: 60/056,875	
41	EARLIER FILING DATE: 1997-08-22	
42	EARLIER APPLICATION NUMBER: 60/056,862	
43	EARLIER FILING DATE: 1997-08-22	
44	EARLIER APPLICATION NUMBER: 60/056,887	
45	EARLIER FILING DATE: 1997-08-22	
46	EARLIER APPLICATION NUMBER: 60/056,908	
47	EARLIER FILING DATE: 1997-08-22	
48	EARLIER APPLICATION NUMBER: 60/048,964	
49	EARLIER FILING DATE: 1997-06-06	
50	EARLIER APPLICATION NUMBER: 60/057,650	
51	EARLIER FILING DATE: 1997-09-05	
52	EARLIER APPLICATION NUMBER: 60/056,884	
53	EARLIER FILING DATE: 1997-08-22	
54	EARLIER APPLICATION NUMBER: 60/057,669	
55	EARLIER FILING DATE: 1997-09-05	
56	EARLIER APPLICATION NUMBER: 60/049,610	
57	EARLIER FILING DATE: 1997-06-13	
58	EARLIER APPLICATION NUMBER: 60/061,060	
59	EARLIER FILING DATE: 1997-10-01	

Query Match 2.1%; Score 35.4; DB 4; Length 1541;
Best Local Similarity 52.3%; Pred. NO. 0.48;
Matches 78; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

1537	QY	AAAATAATATGTTAGTAGTTTGGCTCTTCGTAAACTATCTGGGTGCTAAATCCAAATGAG	1596
1389	Db	AATATGTTACATATGGATTTTTTTATGTGTAGATTTAAACAGCTTTTAAAATCTCTGTTT	1448
1597	QY	AATGCTTTATGTCTAAACCTTCATGAATCTCTCTATCTACATCTTTCAATCTAATACA	1656
1449	Db	TCGTGACAGCTGTTAGAAGTTTGTGATTTCTCCAAATATGCCTAGATTTTAAAGCTGATTA	1508
1657	QY	TATGAGCTCTTCCAAAAAATAAAAAAAAAA	1685

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Db 1509 ATTTATGGAAAAA 1537
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RESULT 13
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEFFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOU
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 50
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent'n Release #1.0, Ver
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
; US-08-232-463-14

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Query Match          2.1%; Score 35.4; DB 1; Length 7218;
Best Local Similarity 10.9%; Pred. No. 1.3;
Matches 30; Conservative 127; Mismatches 118; Indels 0; Gaps 0;

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[illegible]

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 08:21:37 ; Search time 316 Seconds

(without alignments)
15737.557 Million cell updates/sec

Title: US-09-854-562-1

Perfect score: 1685
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Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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10	722.2	42.9	86014	8	F19C14	F19C14
11	721.2	42.8	5798	8	AF031649	AF031649
12	558.8	33.2	1157	8	STXAP1	STXAP1
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26	507.2	30.1	1867	8	ATDBAP3	ATDBAP3
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ALIGNMENTS

RESULT 1
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DEFINITION Sequence 1 from Patent WO9401559.
ACCESSION A37879
VERSION A37879.1 GI:2294549
KEYWORDS
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 1685)
REFERENCE
AUTHORS Frommer, W.
TITLE DNA SEQUENCES FOR AN AMINO ACID TRANSPORTER, PLASMIDS, BACTERIA.

Pred. No. is the number of results predicted by chance to have a

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Db	1621	GAATCTCTCTGATCTACATCTTTCAATCTAATACATATGAGCTCTTCCAAAAA	1680
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Db	1681	AAAAA 1685	
RESULT 6			
LOCUS	ATHTAT	1665 bp	linear
DEFINITION	Arabidopsis thaliana amino acid transporter mRNA, complete cds.	PLN 30-SEP-1993	
ACCESSION	L16240		
VERSION	L16240.1	GI:404018	
KEYWORDS	amino acid transporter.		
SOURCE	Arabidopsis thaliana cDNA to mRNA.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
AUTHORS	1 (bases 1 to 1665)		
TITLE	Hou, L. C., Chiu, T. U., Chen, L. and Bush, D. R.		
JOURNAL	Cloning a plant amino acid transporter by functional		
MEDLINE	complementation of a yeast amino acid transport mutant		
PUBMED	Proc. Natl. Acad. Sci. U.S.A. 90 (16), 7445-7445 (1993)		
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ORIGIN			
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DB 8360 CCAAAACCAAGAGAGATCGTTTTTTTTTCTCACTTTCATGATGTTGGCTAATGAAA 8419


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VERSION AC008051.3 GI:7462019
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SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 86014)
Liu, S.X., Sakano, H., Yu, G., Lee, J.M., Lenz, C., Pham, P., Toriumi, M.,
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Conn, L., Conway, A.B., Hansen, N.F., Johnson-Hopson, C., Khan, S.,
Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P.,
Southwick, A., Davis, R.W., Ecker, J.R., Federspiel, N.A. and
Theologis, A.
The sequence of BAC F19C14 from Arabidopsis thaliana chromosome 1
Unpublished
2 (bases 1 to 86014)
REFERENCE
Theologis, A.
Direct Submission
Submitted (16-JUL-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
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REFERENCE
Theologis, A.
Direct Submission
Submitted (06-APR-2000) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
4 (bases 1 to 86014)
Theologis, A.
Direct Submission
Submitted (08-JUL-2000) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
On Apr 6, 2000 this sequence version replaced gi:6814962.
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Cloning a plant amino acid transporter by functional
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Proc. Natl. Acad. Sci. U.S.A. 90 (16), 7441-7445 (1993)
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VERSION AJ007574.1 GI:3293030
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Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
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REFERENCE
AUTHORS Neelam,A.
TITLE Direct Submission
JOURNAL Plant Biochemistry and Biotechnology, Leeds, LS2 9JT, UNITED
KINGDOM
2 (bases 1 to 1500)
REFERENCE
AUTHORS Marvier,A., Neelam,A., Bick,J.A., Hall,J.L. and Williams,L.E.
TITLE Cloning of a cDNA coding for an amino acid carrier from Ricinus
communis (RcAAP1) by functional complementation in yeast: kinetic
analysis, inhibitor sensitivity and substrate specificity
JOURNAL Biochim. Biophys. Acta 1373 (2), 321-331 (1998)
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 AUTHORS 1 (bases 1 to 1136)
 TITLE Scholze, W., Frommer, W.B. and Ward, J.M.
 JOURNAL Transporters for ammonium, amino acids and peptides are expressed
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 AUTHORS 2 (bases 1 to 1136)
 TITLE Scholze, W., Frommer, W.B. and Ward, J.M.
 JOURNAL Direct Subcellular
 REFERENCE Submitted (29-JUL-1998) Plant Physiology, University of Tuebingen,
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 Fischer, W.N.
 DIRECT SUBMISSION
 TITLE Submitted (02-DEC-1998) W.N. Fischer, IGF, Institut f.
 JOURNAL Genbiologische Forschung, Ihnestr. 53, 14195, Berlin, FRG
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 Fischer, W.N., Kwart, M., Hummel, S. and Frommer, W.B.
 REFERENCE Substrate specificity and expression profile of amino acid
 AUTHORS transporters (AAPs) in Arabidopsis
 TITLE J. Biol. Chem. 270 (27), 16315-16320 (1995)
 JOURNAL 9532342
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 PUBMED
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Sun Dec 1 18:14:46 2002

us-09-854-562-1.rge

Page 19

Search completed: December 1, 2002, 10:00:30
Job time : 3370 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 07:35:02 ; Search time 267 Seconds
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Listing first 45 summaries

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5	501.6	29.8	1759	21	AAQ36303
6	445.4	26.4	1375	21	AAQ41523
7	362.8	21.5	1404	21	AAQ48418
8	191.6	11.4	660	24	ABQ65898
9	77.6	4.6	492	21	AAQ37796

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ALIGNMENTS

RESULT 1	AAQ55058	standard; cDNA; 1685 BP.
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DE	Amino acid transporter; AAT; plant transformation; ss.	
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XX	XX	(GENB-) INST GENBIOLOGISCHE FORSCHUNG.
XX	XX	Frommer W;
XX	XX	WPI; 1994-017036/03.
XX	XX	P-PDB; AAR47812.

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Reference sequence
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Chemically treated
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Signal transductio
Human chemically m
Human immune syste
Genomic sequence #
Genomic sequence #
Genomic sequence #
Arabidopsis thalia
Signal transductio
Human cancer assoc
Porcine BAC-PIGF2-
Genomic sequence
Chemically treated
Human gene regulat
Rat glyceraldehyde
Drosophila melanog
Human ovarian and
Human reproductive
Soybean sucrose tr
cDNA encoding a bo
Human secreted pro
Tumour suppressor
Human chemically p
Human immune syste

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KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
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DB 332 TTGATGACGATGGCGGGCTTAAAGCTTCAGGACGGTTTGGACCGGAGTCCGATATCA 391
QY 202 TCACGGCGGTGATAGGCTCCGGAGTGTGTCTTTAGCATGGGCTATAGCTCAGCTTGGTT 261
DB 392 TAAACCGCGTGAATTGGATCTGCTGTCTATCGCTTGGTGGGCTATAGGTCAACTCGGTT 451
QY 262 GGATCGCAGGAGACATCGATCTTACTCATTTTCTGTTCAATTACTTACTTACCTCCACCA 321
DB 452 GGATCGCAGGCTTACAGTGTATGTTGTTCTCTCTTTGTCTACTTACTTCTTCCACGC 511
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QY 382 TGGACGTTTGTTCGATCTTACCTCGGTGGTAGGAAAGTCAGCTCTGTGGAGTGGCACAAT 441
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QY 442 ATGGGAATCTGATTTGGGGTCACTGTTGGTTACACATCAGCTGCTTCTATTAGTTGGTAG 501
DB 632 ATTTGAATCTGTTGGTATCACGGTCGGGTACACAATCGCAGCATCTATAAGTAGTAGTG 691
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QY 562 ATTATCCGTATATGCGGGTTTTGGTATCAATCAAGTTATTCTTTAGCCAGATCCCAAT 621
DB 752 GCAATCCATACATGATCATGTTTGGTGTGACCGAGATCTTGCTCTCTCAGATCAAGATT 811
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QY 802 CGGTTGGGACATAGCGTTTCGCTTATGCTTATGCGCAGGTTCTCATCGAGATTCAGGATA 861
DB 989 CACTTGGAGACATTCGCTTTGCTTTATTATATATCTGTTGTTCTTTATTGAAATTCAGGACA 1048
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DB 1049 CTGTAAGATCTCCACAGCAGAAATCAAAACGATGAAGATCGCCACAGAAATCAGATCG 1108
QY 922 CAACCAACCACTTTTCTTACATCTTATGTGATGATCGCTATGCTGCTGCAATTTGGAACA 981
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QY 982 ATGCCCTGGAGATTTCCTCAGATTTTCGGGTTTTTCGAGCCCTTTTGGCTCATTTGACT 1041
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QY 1102 TATTCCAGTTTGTGAGAAAAAATGCAACAGAAACTATCCAGACAAAGTTTCATCACTT 1161
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DB	220	AAATGCTTCGATGATGCGCGCTCAAAGAACTGGGACTGTTGGACCGCGAGCGCT 279
QY	195	CATATTATCAGCGGCGTATAGGCTCCGGAGTGTGCTTTTAGCATGGGCTATAGCTCAG 254
DB	280	CATATAAATACTGGCGTTATCGGATCCGGCGTTTTGTTCATTGGCGTGGCGGATTCACAG 339
QY	255	CTTGGTTGGATCGGAGGACATCGATCTTACTCATTTTCTCGTTTCATTACTTACTTACC 314
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QY	315	TCCACATGTTGGCGATTGCTACCGTGGCGCGGATCCGTCACCGGAAAAACGGAATTAC 374
DB	400	TCCACACTTCTTAGCGACTGCTACAGAACCGGCGATGCGAGTGTCTGGCAAGAGAACTAC 459
QY	375	ACTTACATGGAGGTTGTTTCGATCTTTACCTCGGTGGTAGGAAGTGCAGCTCTGTGGAGTG 434
DB	460	ACTTACATGGAGTGGCTTCGATCAATTCCTCGGTGGGTTCAAGTTCAGATTTGTGGGTTG 519
QY	435	GCACAATATGGAAATCTGATTTGGGGTCACTCTTGGTTACACCATCACTGCTTCTATTAGT 494
DB	520	ATTCAATACCTTGAATCTCTTTGTTATCGCAATGGATACACGATAGCAGTTCCTAATAGC 579
QY	495	TTGGTAGCGGTAGGAAATCGAACTGCTTCCACGATAAAGGCGCACACTGCGGATTTGTACT 554
DB	580	ATGATGGCGATCAAGAGATCCAACTGCTTCCAAAGAGTGGAGGAAAGACCCATGTAC 639
QY	555	ATATCGAATTATCCGTATATGCGCGTTTTTGGTATFCATFTCAAGTATTTCTTAGCCAGATC 614
DB	640	ATGTCAGTAATCTTACATGATCGTATTTGGTGTGGCAGAGATCTTGTCTCTCAGGTT 699
QY	615	CCAAATTTCCACAAGCTCTCTTTTCTTCCATTTATGGCCGCGAGTCATGCTCTTTACTTAT 674
DB	700	CCTGATTTTCGATCAGATTTGGTGGATCTCCATTTGTGCGAGCTGTATGTCTCTTCACTTAC 759
QY	675	GCACTATTGGAAATCGGTCTAGCCATCGAACCGTCGAGGTGGGAAAGTGGGTAAGACG 734
DB	760	TCTGCCATTGGTCTAGCTCTTTGGAAATCGTTCAAGTTGCGGGAATGGAGTTTTCNAAGGA 819
QY	735	AGTATGACGGGCACAGCGGTTGGAGTAGATGTAAACCGCAGCTCAAAAGATATGGAGATCG 794
DB	820	AGTCTCACTGGAATAAGCATCGGAACA---GTGACTCAACACAGAGATATGGAGAACC 876
QY	795	TTTCAAGCGGTTGGGACATAGCGTTCCGCTATGCTTATGCCAGGTTCTCATCGAGATT 854
DB	877	TTCCAAGCACCTTGGAGACATTTGCCCTTTGCGTACTCATACTCTGTTGCTCTAATCGAGATT 936
QY	855	CAGGATACACTAAGATCTAGCCCGAGCTGAGAAACAAAGCATGAAAGAGCAAGTCTTCTGTG 914
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QY	193	CGCATATTATCAGGGGGTGATAGGCTCGGAGTGTTCTCTTTAGCATGGGTATAGCTC 252
DB	254	CACACATAATAACGGCAGTGATAGGTTCCGGAGTGTGTCTACTAGCTGGGTACGGCGC 313
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DB	314	AGCTAGGTGGCTCGCCGACCGGTGGTGTGCTCTTCTCTGCGCTCACTTATTTC 373
QY	313	CCTCCACCATGCTTCCGATTTGCTACCGTGGCGCGGATCCCGTACCGGAAACCGAAAT 372
DB	374	CTTCTTCTCTTCTGCTGCTTTTACCGCTCGGGGACCCCTATCTCCGCAAGAGNACT 433
QY	373	ACATTACATGAGCGTTGTTTCGATCTTACCTCGGTGGTAGAAAGTGAGCTCTGTGGAG 432
DB	434	ACACTTATATGGATGCTGCCGATCAAACTCTCGGTGGCGTGAAGGTGACGCTATGTGG 493
QY	433	TGGCACAATATGGGAATCGATTCGGGTCACTGTGGTTTACCATCACTCACTCTTCTATTA 492
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QY	493	GTTTGGTAGCGTAGGAAATCGAACTGCTTCCACGATAAAGGGCACACTCGGATTTGTA 552
DB	554	GCATGATGCAATAAAGAGATCAAACTGTTTCCACAAGAGTGGAGGAAGATCCATGTC 613
QY	553	CTATATCGAAATTCCTGGTATATGGCGGTTTTTGGTATCATTTCAAGTTATCTTTAGCCAGA 612
DB	614	ACATGAACAGTAATCCTTACATGATAGCTTTTGGATTAGTCCAGATTCTATTCTCTCAGA 673
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QY	673	ATGCAACTATTGGGAATCGGTCTAGCCATCGCAACCGTCCGAGGTGGGAAAGTGGTAAGA 732
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DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 57407.
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XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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OS Arabidopsis thaliana.
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PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 21.5%; Score 362.8; DB 21; Length 1404;
Best Local Similarity 57.1%; Pred. No. 4.7e-99;
Matches 752; Conservative 0; Mismatches 542; Indels 24; Gaps 4;

QY 166 GTACCGGAGCGTGGCTTACGGCGAGTGGCATATTATCACGGCGGTATAGGCTCCGGAG 225
DB 77 GAACAGGAACGTTATGGACGGCGGTGGCACATATATACAGGAGTATAGGAGCTGGAG 136

QY 226 TGTTCCTTTAGCATGGCTATAGCTCAGCTTGGTTGGATCGCAGGAGACATCGATCTTAC 285
DB 137 TGTTCCTTGGCTTGGCCACGGCGGAGCTCGGCTGGATCGTGGTCCGGCCGCCCTTA 196

QY 286 TCATTTTCTCGTTCACTTACTTACCTCCACCATCTTCCCGATCTTCCGATTTCTACCTGGCC 345
DB 197 TAGCCTTCGCCGGGTACACTTCTCTGCTTTTCTTTTCGATTTGCTACCGCTTCC 256

QY 346 CGGATCCCGTCACCGG---AAAACGGAATTACACTTACATGACGCTTGTTCGATCTTACC 402
DB 257 CTGATCCTAACACACGCTCCCTCCGACTCAATTTCTTACTCTCAAGCCGTTAAATTTGATT 316

QY 403 TCGTGGTAGGAAAGTCAGCTCTGTGGAGTGGCAATATGGGAATCTGATTTGGGTCA 462
DB 317 TAGGGAAGAAGAAATGATGTGGAGTCGTTGTATACATTTCCCTTTTGGTTGTG 376

QY 463 CTGTTGGTTACACCATCACTGCTTCTATTAGTTTGGTAGCGGTAGGGAANTCGAACTGCT 522
DB 377 GCATTTGCTTATACCAATTTTATAGCTACATGAGTACAGTATGAAATCGAATTTGTT 436

QY 523 TCCAGATAAAGGGCACACTCGGATTGTAC-----TATATCGAATTTATCGTATATGG 576
DB 437 ATCATAGAAATGGACAAATGCAACATGTTATATGGAGACAAACAACTACTTCTATGG 496

QY 577 CGGTTTTTGGTATCATTTCAAGTTATTTCTTAGCCAGATCCCAAATTTCCACAGCTCTCTT 636
DB 497 TTTTGTGTTGGTTGACTCAGATATTTATGTCACAAATACCTAAATTTCCACAACTGGTAT 556

QY 637 TTCTTTCCATTTATGGCCGAGTCATGCTCTTTACTTATGCAACTTATTTGGAATCGGTCTAG 696
DB 557 GGCTCTCTCTTGTGCCGCTATTATGCTTTTACTTACTCGTTTCTATTTGGCATCGGCCCTCG 616

QY 697 CCATCGCAACCGTCGACGTTGGGAAGTGAACAGGATGACGGGACACAGCGGTTG 756
DB 617 CCCTTGGCAAAATCATAGAAATCGAAAAATTTAGGGGAAGTATAGGGGAATACC----- 671

QY 757 GAGTAGATGTAACCGCAGCTCAAAAGATATGAGATCGTTTCAAGCGGTGCGGGACATAG 816
DB 672 ---AGCAGAAAAACAGAGGTGAAAGGTTATGGATAGTGTTCACAGCTCTTCCGACATTTG 727
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QY 817 CGTGGCCCTATGCTTATGSCACGGTTCATGAGATTCAGATTAAGTCTAGCC 876
 DB 728 CCTTTTCATATCTTCTTCAATCATCTACTTCTTGAGATTCAGACATGAGATCACAC 787
 QY 877 CAGCTGAGAAACAAGCCATGAAAAGCAAGCTTGTGGAGATATACACCACTTTT 936
 DB 788 CGGCGAGAGAGAAACGATGAAGAAAGCCCTCGACGGTTCGGTATTCACAAACATTTCT 847
 QY 937 TCTACATCTTATGATGATCATCGCTATGCTGATTCGATTTGGAACAATGCCCTGAGATT 996
 DB 848 TCTTCTCTGTTGTGATTTTGGGTACGGCCCTTTGAGATTCACCCCGGAAATC 907
 QY 997 TCCCTACAGATTTGGGGTTTTGAGCCCTTTTGCTCATTTGACTTTGCAAAAGCTTTGA 1056
 DB 908 TCTTGACCGGTTTCGGCTTCTATGACCAATTCGGCTCGCATTTGCGCAAGCTTTGA 967
 QY 1057 TCGCTGTCCACCTTATGCTGTGCTATCAGGTGTGCGGACCGGATATTCAGATTGTTG 1116
 DB 968 TTGTTCTTCATTTAGTTGGTGTATCAGGTATACAGTCAACCAATTTTCGGCGCTGG 1027
 QY 1117 AGAAAAATGCAACGAACCTATCCAGACACAGTTCATCACTTCTGAATATTCAGTAA 1176
 DB 1028 AAGATCGCTAACCAAGAAATATCCGAAATATGATTATTCGACAGATTCTACGATTCA 1087
 QY 1177 ACGTACCTTTCCTTGA-----AAATTCACATTAGCCTTTGAGATTGTTGAGGA 1230
 DB 1088 AACTGCATTGTTGGAGAGAGAGAGAGAGTGAAGTGAACCAATGAGAGTGTGTAGAA 1147
 QY 1231 CAGCTTATGTGTTATACCACTGTTTGAAGTATGATATTTCCCTTTTCAACGCACTCT 1290
 DB 1148 CATGTACCTGTTGATCAACACGGAGTGCAGTGTATGTTCCCTTCAATGAAGTAT 1207
 QY 1291 TAGTCTTATCGAGAGAGCTTCTTGGCCTTAAAGGTTATTTCCCTGTGAGATGC 1350
 DB 1208 TAGGAGTGTGGGGGACATTGCAATTTGGCTCTGCGAGTATTTCCGTGAGATGT 1267
 QY 1351 ACATTGCACAAACAAGATTAGAACTACTGCTAGATGATTTGGCTGAAGAAAGATGT 1410
 DB 1268 GATATATGCAAGAAATCCGAAGTTGACGCGACATAGCTTCTTTAGAGTTCA 1327
 QY 1411 GCTATGTTGCTTATGCTGCTCTCTTAACTGACCGCGATTCGACAGACTTAT 1468
 DB 1328 GCTTGTGTGCTGTGCTGCTGCTCTGCTCTTGTGATCTATTTAGACTTGT 1385

RESULT 8
 ABO65898
 ID ABO65898 standard; DNA; 660 BP.

AC ABO65898;
 DT 21-AUG-2002 (first entry)
 DE Arabidopsis thaliana polynucleotide SEQ ID NO 475.
 XX Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease;
 KM stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide;
 KM insecticide; antibiotic; ds.
 OS Arabidopsis thaliana.
 PN US2002059663-A1.
 PD 16-MAY-2002.
 PF 26-JAN-2001; 2001US-0770149.
 PR 27-JAN-2000; 2000US-178506P.
 PA (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HAMI/) HAMILTON C M.

PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUY/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHEN A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRICK/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 PI Goriach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y,
 PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD,
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
 PI Hurban P;
 DR WPI; 2002-479224/51.
 XX
 PT New nucleic acid that hybridizes to Arabidopsis thaliana sequences,
 PT useful e.g. for preparing transgenic plants with increased resistance
 PT or altered metabolism -
 PS Claim 1; SEQ ID NO 475; 40pp + Sequence Listing; English.
 XX
 CC The invention relates to nucleic acids (i) that hybridise under stringent
 CC conditions to any of 999 sequences (ABO65424-ABO66422) or their
 CC fragments. (ii) are used to express the corresponding polypeptides (ii) or
 CC to produce genetically modified plant cells or transgenic plants, which
 CC may have improved resistance to disease or stress, or altered
 CC metabolic/biosynthetic pathways (for production of commercial,
 CC nutritional or medicinal products), or generally any trait of interest,
 CC or can be used to screen for biologically active agents (e.g. fungicides,
 CC insecticides and antibiotics).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC USPTO at seqdata.uspto.gov/sequence.html?docid=99909770149.
 CC
 SQ Sequence 660 BP; 179 A; 118 C; 165 G; 198 T; 0 other;

Query Match 11.4%; Score 191.6; DB 24; Length 660;
 Best Local Similarity 61.6%; Pred. No. 2.4e-47;
 Matches 324; Conservative 0; Mismatches 199; Indels 3; Gaps 1;

QY 981 AATGCCCTGAGATTTCTCACAGATTCGGGTTTTCGAGCCCTTTGGCTCATTGAC 1040
 DB 1 AAGACACCGGAAACCTCTTAAACGGTTTGTTTACAAATTCGTTTGCTCTTGAC 60
 QY 1041 TTGCAAGCCTTGATCGCTGTCCACTTATTTGATGCTATCAGGTGTGCGACCG 1100
 DB 61 GTGGTAAAGCTGCCATGATTTATCCACTTTGAGAGCTTATCAAGTCTTGTCAGCC 120
 QY 1101 ATTTTCAAGTTTGTAGAAAAATGCAACAGAAATATTCAGACAAAGTTCACT 1160
 DB 121 ATCTTGCCCTTATTTAGAAACAAAGCTGCCGTAGGTTTCCGACAGTGACTTGGTACC 180
 QY 1161 TCTGATTTTCAGTAAGTACCTTCTTGG--AAATTCACATTTAGCCCTTCAGA 1217
 DB 181 AAGAAATACGAATCCGAATCCCTGTTTATGATCACCGTACAAAGTCAAGTTTCAGA 240
 QY 1218 TTGCTGTGAGAGACAGCTTATGTTATTAACCACTGTGTAGCTATGATTTCCCTTTC 1277
 DB 241 GAGTTTACGAAGCGGTTTGTGTTTGACACATGTATATCATGCTATGCGGTTT 300
 QY 1278 TTCAAGCGATCTTATGCTTATCGAGACGCTTCTTCTGCGCTTTAAGCTTTATTTT 1337
 DB 301 TTCAACAGAGCTGTAGGATTTTATGAGTGTGCTTAAAGGTTTGGCTTTGACGTTTACTT 360

PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144335.
PR 19-JUL-1999; 99US-0144335.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 16-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.

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PR 29-OCT-1999; 99US-0162142.
Query Match 4.5%; Score 76; DB 21; Length 485;
Best Local Similarity 61.7%; Pred. No. 2,2e-12;
Matches 121; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 166 GTATCCGGACGCTGAGCTTACGCGACAGTCCGATTTATCAGCGCGGTGATAGCTCCGAG 225
DB 120 GAACACAGAACGTTATGAGACGCGCGGTGACATTAATACAGAGATGATAGAGCTGAG 179
QY 226 TGTGTCTTAGCATGCGCTATGCTCAGCTTGTTGATCGAGGAGACATCATCTTAC 285
DB 180 TGTGTCTTAGCTTGTTGCGGACGCGAGCTCGCTGATCGTGTCCGCGCCCTTA 239
QY 286 TCATTTTCTGTTCTTACTTACTTACTTCACTTCCACCATGTTGCGGATGCTACCGCGC 345
DB 240 TAGCCTTCCGCGGCGGACACACTTCTCTGCTTTCTTCTTCCGATGCTACCGTTTC 299
QY 346 CCGATCCCGTCAACCG 361
DB 300 CTGATCTTAACAACGG 315

RESULT 11
AAD02471
ID AAD02471 standard; cDNA; 1882 BP.
AC AAD02471;
XX
XX
XX 24-APR-2001 (first entry)
DE cDNA clone bchl.pK0013.h9, encoding barley LHT1.
XX
XX
XX Barley; lysine- and histidine-specific transporter; LHT1;
XX proline transporter; transgenic plant; immunological screening; ss.
XX
XX Hordeum vulgare.
OS
XX
XX
XX Key Location/Qualifiers
XX CDS 70..1413
XX FT /tag= a
XX FT /product= "Barley LHT1 protein"
XX
XX US6165792-A.
XX
XX
XX 26-DEC-2000.
XX
XX
XX 09-AUG-1999; 99US-0370253.
XX
XX
XX 20-AUG-1998; 98US-0097222.
XX
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E. I.
XX
XX Thopre CJ, Allen SM;
XX
XX WPI; 2001-090485/10.
XX
XX P-PSDB; AAY72391.
XX
XX
XX Nucleic acids encoding amino acid transporters, e.g. lysine- and
XX histidine-specific transporter and proline transporter, useful for
XX transgenic plant production with altered expression level of the amino
XX acid transporters -
XX
XX
XX Claim 3; Column 19-22; 24pp; English.
XX
XX
XX The present cDNA sequence encodes barley lysine- and histidine-specific
XX transporter (LHT1) from clone bchl.pK0013.h9, isolated from a barley
XX sheath or developing seedling tissue of bchl cDNA library.
XX The invention relates to lysine- and histidine-specific transporter
XX (LHT1), proline transporter and their corresponding cDNA clones. It is
XX useful for producing transgenic plants with altered expression level of
XX amino acid transporters, in cell types or developmental stages in which
XX they are not normally found, such that the obtained transgenic plants

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CC show increased tolerance to salt and water stresses. The level of lysine,
CC histidine and proline in cells of the transgenic plant, is also altered.
CC The invention is also used for constructing a chimeric gene encoding all
CC or a portion of the amino acid transporter, where in the expression of
CC chimeric gene results in the production of altered levels of amino acid
CC transporter in a transformed host cell. Synthetic peptides obtained from
CC LHT1 and proline transporter are used for immunising animals to produce
CC polyclonal or monoclonal antibodies, which facilitates the immunological
CC screening of cDNA expression libraries.
XX
XX
XX Sequence 1882 BP; 475 A; 488 C; 466 G; 453 T; 0 other;
XX
XX
XX Query Match 3.2%; Score 53.2; DB 22; Length 1882;
XX Best Local Similarity 51.1%; Pred. No. 3.7e-05;
XX Matches 183; Conservative 0; Mismatches 163; Indels 12; Gaps 2;

QY 768 ACCGAGCTCAAAAGATATGAGATGCTTCAAGCGGTGGGACATAGCGTCTAT 827
DB 730 ACGACAGCAGGCGAGGTGTTGTTCTTGGGGGCGCTCGCATGATGATCTCTAC 789
QY 828 GCTTATGCCACGGTCTCATCGAGATTTCAGATACATAAGATCTAGCCAG-----CT 881
DB 790 TCCGGCCACAAATGTGTGCTAGAAATTCAGGCTACCATCCATCGACGCCGCAACCG 849
QY 882 GAGAACAAAGCCATGAAAAGAGCAAGCTTTGTGGAGATCAACCAACTTTTCTAC 941
DB 850 TCCAGAGCCAAATGTGGAAGGCGTGTGTGCTTACATCATATCGCGCTGTAC 909
QY 942 ATCTTATGTGATGATCGCTATGCTCATTTTGGAAACAATGCCCTGAGATTTCCTC 1001
DB 910 TTCCGGTGGCATTTATCGCTACTGAGCAATTTGGCAACGCGCTGACGCAACATCCTC 969
QY 1002 ACAGATTTGGGTTTTCGAGCCCTTTGGGCTCATTTGATTCGCAACGCTTGATGCT 1061
DB 970 A-----TACCTTCAACAGAACCCAAAGTGTCTATGCTTCCCAACATGATGCTGTC 1023
QY 1062 GTCCACCTTATTTGTCCTATACAGTGTTCGCGACCGCATATTCAGTTTGTGAGA 1119
DB 1024 GTTCACCTCATGTGTGCTACACGATTTTATGGATGCCGCTGTTGATCATGATGAGA 1081

RESULT 12
AAD02472
ID AAD02472 standard; cDNA; 1016 BP.
AC AAD02472;
XX
XX
XX 24-APR-2001 (first entry)
XX
XX
XX cDNA clone ctain.pK0048.h2, encoding corn LHT1.
XX
XX
XX Corn; lysine- and histidine-specific transporter; LHT1;
XX proline transporter; transgenic plant; immunological screening; ss.
XX
XX
XX Zea mays.
XX
XX
XX Key Location/Qualifiers
XX CDS 2..781
XX FT /tag= a
XX FT /product= "Corn LHT1 protein"
XX FT /note= "Does not include start codon"
XX
XX
XX US6165792-A.
XX
XX
XX 26-DEC-2000.
XX
XX
XX 09-AUG-1999; 99US-0370253.
XX
XX
XX 20-AUG-1998; 98US-0097222.
XX
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E. I.
XX

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PI Thopre CJ, Allen SM;
XX WPI; 2001-090485/10.
DR P-PSDB; AAY72392.
XX Nucleic acids encoding amino acid transporters, e.g. lysine- and
PT histidine-specific transporter and proline transporter, useful for
PT transgenic plant production with altered expression level of the amino
PT acid transporters -
XX Claim 3; Column 23-26; 24pp; English.
PS The present cDNA sequence encodes corn lysine- and histidine-specific
XX transporter (LHT1) from clone ctain.pk0048.h2, isolated from a corn
CC tissue ctain cDNA library.
CC The invention relates to lysine- and histidine-specific transporter
CC (LHT1), proline transporter and their corresponding cDNA clones. It is
CC useful for producing transgenic plants with altered expression level of
CC amino acid transporters, in cell types or developmental stages in which
CC they are not normally found, such that the obtained transgenic plants
CC show increased tolerance to salt and water stress. The level of lysine,
CC histidine and proline in cells of the transgenic plant, is also altered.
CC The invention is also used for constructing a chimeric gene encoding all
CC or a portion of the amino acid transporter, where in the expression of
CC chimeric gene results in the production of altered levels of amino acid
CC transporter in a transformed host cell. Synthetic peptides obtained from
CC LHT1 and proline transporter are used for immunising animals to produce
CC polyclonal or monoclonal antibodies, which facilitates the immunological
CC screening of cDNA expression libraries.
XX Sequence 1016 BP; 203 A; 294 C; 269 G; 250 T; 0 other;
SQ Query Match 3.1%; Score 51.6; DB 22; Length 1016;
Best Local Similarity 50.8%; Pred. No. 8.2e-05;
Matches 182; Conservative 0; Mismatches 164; Indels 12; Gaps 2;
QY 768 ACCGAGCTCAAAAGATATGGAGATCGTTTCAAGCGGTTGGGACATAGCGTTCGCTAT 827
DB 98 ACCAGCCGGGGAAGGTGTTCGGCTTCCTTGGCGCGCTGGGGACGTGGCGTTCGCTAC 157
QY 828 GCTTATGCCACCGTTCATCGAGATTCAGGATACACTAAGATCTAGCCCCAGCTGAG--- 884
DB 158 GCGGCCCAACAGTGTGTGGAGATCCAGGCCACCATCCCGTCCACCCCGCAAGCCG 217
QY 885 ----AACAAGCCATGAAAAGAGCAAGTCTTGTGGAGATATCAACACCACTTTTTCATC 941
DB 218 TCCAAGAGCCCATGGAAGGCGGTGTGTCGCTACGTGTCGCTGCTGCTAC 277
QY 942 ATCTTATGTGGATGATCGCTATGCTGATTTGGAACAATGCCCTGGAGATTCCTC 1001
DB 278 TTCCCGCTCGCTCATCGGCTACTGGCGTTTCGGAACAACCGGTGAGGACAACATCCTC 337
QY 1002 ACAGATTTTCGGGTTTTCGAGCCCTTTTCGGCTCATTGACTTTTGCAACGCTTGCATCGCT 1061
DB 338 A-----TCACCTAGCAAGCCCAAGTGGCTCATCGCGCTGCCAACATGATGTGCTC 391
QY 1062 GTCCACCTTATTTGGTCCCTATCAGGTGTTTCGGCGAGCCGATATTCAGTTTGTGAGA 1119
DB 392 GTCCATGTATCGGAGCTACCAAGATCTATGCCATGTCGCGGTGTTGACATGATAGAGA 449
RESULT 13
AAD02473
ID AAD02473 standard; cDNA; 1865 BP.
XX AC
AC AAD02473;
XX 24-APR-2001 (first entry)
DE cDNA clone rls48.pk0011.g8, encoding rice LHT1.
DE Rice; lysine- and histidine-specific transporter; LHT1;
KW proline transporter; transgenic plant; immunological screening; ss.
KW
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XX Oryza sativa.
OS
XX Key Location/Qualifiers
FH 112..1455
FT /*tag= a
FT /product= "Rice LHT1 protein"
XX
XX US6165792-A.
XX 26-DEC-2000.
XX 09-AUG-1999; 99US-0370253.
XX 20-AUG-1998; 98US-0097222.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Thopre CJ, Allen SM;
XX WPI; 2001-090485/10.
XX P-PSDB; AAY72393.
XX Nucleic acids encoding amino acid transporters, e.g. lysine- and
PT histidine-specific transporter and proline transporter, useful for
PT transgenic plant production with altered expression level of the amino
PT acid transporters -
XX Claim 3; Column 25-28; 24pp; English.
PS The present cDNA sequence encodes rice lysine- and histidine-specific
CC transporter (LHT1) from clone rls48.pk0011.g8, isolated from a rice
CC leaf tissue rls48 cDNA library.
CC The invention relates to lysine- and histidine-specific transporter
CC (LHT1), proline transporter and their corresponding cDNA clones. It is
CC useful for producing transgenic plants with altered expression level of
CC amino acid transporters, in cell types or developmental stages in which
CC they are not normally found, such that the obtained transgenic plants
CC show increased tolerance to salt and water stress. The level of lysine,
CC histidine and proline in cells of the transgenic plant, is also altered.
CC The invention is also used for constructing a chimeric gene encoding all
CC or a portion of the amino acid transporter, where in the expression of
CC chimeric gene results in the production of altered levels of amino acid
CC transporter in a transformed host cell. Synthetic peptides obtained from
CC LHT1 and proline transporter are used for immunising animals to produce
CC polyclonal or monoclonal antibodies, which facilitates the immunological
CC screening of cDNA expression libraries.
XX Sequence 1865 BP; 439 A; 517 C; 472 G; 437 T; 0 other;
SQ Query Match 2.8%; Score 47.6; DB 22; Length 1865;
Best Local Similarity 50.6%; Pred. No. 0.0019;
Matches 175; Conservative 0; Mismatches 159; Indels 12; Gaps 2;
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DB 784 AAGGTGTTTCGGCTTCTTCAGCGCGCTGGCGACGTCGCGTTTCGCGTAGCGGGGCACAA 843
QY 840 GTTCTCATCGAGATTCAGGATACACTAAGATCTAGCCCCAGCTGAG-----AACAAAGCC 893
DB 844 GTGGTGTGGAGATCCAGCGCCATCCCGTCGACCGCGGAGAGCCGTCGAAGAGCGG 903
QY 894 ATGAAAGAGCAAGTCTTGTGGGAGTATCAACACCACTTTTTCATCATCTTATGTGGA 953
DB 904 ATGTGGAAGGCGTCTGCTCGCTCATCATCGTCGCGCTCTGCTACTTCCCCGTGCG 963
QY 954 TGCATCGCTATGTCATTTGGAACAATGCCCTGGAGATTCCTCAGAGATTCGCG 1013
DB 964 CTCGTCGATATCTGGCGCTTCGGCAACCAACGTCGACGACAACTCCTCA-----TCACG 1017
QY 1014 TTTTTCGAGCCCTTTTGGCTCATTTGACTTTTCAACACGCTTGCATCGCTGTCCACCTTAT 1073
DB 1018 CTCACGAGCCCAATGCTCATCGCGCTCCGAAACATGATGGTCTCATCTCATCTCATC 1077
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PR	28-OCT-1999;	99US-0161920;
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Best Local Similarity	62.6%;	Pred. No. 0.004;		
Matches 72;	Conservative 0;	Mismatches 43;	Indels 0;	Gaps 0;

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Db	1041	GGCTCATCGCGGAGTATAGTACACTTAAGGTTTACACCGCTTAAGACTA	1095

Search completed: December 1, 2002, 09:02:54
Job time : 287 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using bw model

Run on: December 1, 2002, 08:57:52 ; Search time 69 Seconds

(without alignments)
9404.631 Million cell updates/sec

Title: US-09-854-562-1

Perfect score: 1685

Sequence: 1 CTTAAACATTATTATTC.....TTCCAAAAAAAAAAAAAA 1685

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 341543 seqs, 19255720 residues

Total number of hits satisfying chosen parameters: 683086

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1451.6	86.1	1458	US-09-938-842A-1470	Sequence 1470, Ap
2	722.2	42.9	1446	US-09-938-842A-802	Sequence 802, Ap
3	507.2	30.1	1431	US-09-938-842A-67	Sequence 67, Appl
4	501.8	29.8	1482	US-09-938-842A-1482	Sequence 1482, Ap
5	191.6	11.4	660	US-09-770-149-475	Sequence 475, Ap
6	180	10.7	406	US-09-878-574-376	Sequence 376, Ap
7	149	8.8	382	US-09-878-574-2601	Sequence 2601, Ap
8	135.4	8.0	387	US-09-878-574-3664	Sequence 3664, Ap
9	119.8	7.1	481	US-09-924-035A-35	Sequence 35, Appl
10	101.4	6.0	383	US-09-878-574-103	Sequence 103, Appl
11	94.4	5.6	264	US-09-878-574-5591	Sequence 5591, Ap
12	88.2	5.2	386	US-09-878-574-3794	Sequence 3794, Ap
13	88	5.2	307	US-09-878-574-1977	Sequence 1977, Ap
14	80	4.7	238	US-09-923-876-317	Sequence 317, Appl
15	56.8	3.4	382	US-09-878-574-3185	Sequence 3185, Ap
16	56	3.3	2000	US-09-938-842A-4162	Sequence 4162, Appl
17	53	3.1	360	US-09-878-574-1677	Sequence 1677, Appl
18	52.4	3.1	265	US-09-878-574-7530	Sequence 7530, Ap
19	49.4	2.9	365	US-09-878-574-2526	Sequence 2526, Appl

20	48.6	2.9	322	US-09-878-574-2868	Sequence 2868, Ap
21	48.4	2.9	280	US-09-923-876-6149	Sequence 6149, Ap
22	46.6	2.8	301	US-09-878-574-1241	Sequence 1241, Ap
23	46.6	2.8	313	US-09-878-574-5186	Sequence 5186, Ap
24	44.2	2.6	376	US-09-878-574-406	Sequence 406, Appl
25	41.6	2.5	346	US-09-770-791-760	Sequence 760, Appl
26	41.2	2.4	159	US-09-878-574-9521	Sequence 9521, Ap
27	38	2.3	5005	US-09-764-847-1383	Sequence 1383, Ap
28	38	2.3	13831	US-09-764-847-1385	Sequence 1385, Ap
29	38	2.3	1832	US-09-764-847-1384	Sequence 1384, Ap
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31	37.6	2.2	397658	US-09-813-320-3	Sequence 3, Appl
32	37.4	2.2	449	US-09-933-797-90	Sequence 90, Appl
33	37.2	2.2	2833	US-09-925-301-204	Sequence 172, Appl
34	37	2.2	428	US-09-969-373-1172	Sequence 1172, Ap
35	36.8	2.2	266	US-09-878-574-9185	Sequence 9185, Ap
36	36.2	2.1	1272	US-09-765-205-9	Sequence 9, Appl
37	36.2	2.1	1960	US-09-746-801A-12	Sequence 12, Appl
38	36.2	2.1	3617	US-09-746-801A-14	Sequence 14, Appl
39	35.8	2.1	310	US-09-923-876-3684	Sequence 3684, Appl
40	35	2.1	1813	US-09-732-618-9	Sequence 9, Appl
41	35	2.1	2088	US-09-938-842A-330	Sequence 330, Appl
42	35	2.1	2088	US-09-746-801A-4	Sequence 4, Appl
43	35	2.1	2518	US-09-746-801A-1	Sequence 1, Appl
44	35	2.1	2846	US-10-008-016-1	Sequence 1, Appl
45	35	2.1	4221	US-09-746-801A-3	Sequence 3, Appl

ALIGNMENTS

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RESULT 1
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Sequence 1470, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Krepes, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1470
LENGTH: 1458
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1470

Query Match      86.1% Score 1451.6; DB 9; Length 1458;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1454; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 61 ACCGTGCGACCCGCAAAAGACGTGATGATGCTGAGAGAAAGCTACCGGACG 120
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Db 1441 CGGACTATGCAATGAGTGA 1458
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RESULT 2

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; Sequence 802, Application US/09938842A
; Patient No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krebs, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 802
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-802
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Query Match 42.9%; Score 722.2; DB 9; Length 1446;
Best Local Similarity 71.1%; Pred. No. 6.le-202;
Matches 984; Conservative 0; Mismatches 393; Indels 6; Gaps 2;
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```
QY 126 GACCCGACAAAGAACGTCGATGAAGATGCTCGAGAGAGCGTACCGGACGCTGGCTTACG 185
Db 58 GATACCTAAACAAAACCTTTGACGAGATGCGCGGACAAAAGAACCTGGGACATGGATGACC 117
QY 186 GCGAGTGGCGCATATTATCACGCGCGGTGATAGGCTCCGAGTGTGTCTTTAGCATGGGCT 245
Db 118 GGGAGTGACACATAATAACCGCCGTGATAGGTCGGAGTGTGTCTTTGGCTGGGCA 177
QY 246 ATAGCTCAGCTTGGTGTGATCGCAGGGACATCGATCTTACTCATTTTCTCGTTCACTACT 305
Db 178 ATCGCACAACTTGGATGGTGGCAGGACCCCGCTACTAATGGCTTTTCTTTCTATAACA 237
QY 306 TACTTCACCTCCACCATGCTTGGCCGATGCTACCGTGGCGCGGATCCCGTCACCGGAAA 365
Db 238 TATTTTATCATCAACCATGCTTGGCCGATTTGACCGTTCCCTGACCCCTGTTACCGGCAA 297
QY 366 CGGAATTACACTTACATCGACGTTGTTTCGATCTTACCTCGGTGGTAGGAAAGTCAGCTC 425
Db 298 CGCAACTACACTACATCGAAGTGTCCGATCCTATCTAGGAGGAAGAAAGTGCATTA 357
QY 426 TGTGAGTGGACAAATATGGGAATCTGATTTGGGTCACTGTGGTTACACCATCACTGCT 485
Db 358 TGTGATTTGGCTCAATACGGGAATCTGATTTGGAATAACAAATCGGCTACACAATCACAGCT 417
QY 486 TCTATTAGTTTGGTAGCGGTAGGGAATCGAACTGCTTCCACGATAAAGGGCACACTGCG 545
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Qy	793	CGTTTCAAGCGGTGGGGACATAGCGTTTCGCCCTATGCTTTATGCCACGCGTTCTCATCGAGA	852
Db	713	CCTTTCAAGCTCTTGGAGACATGCTTTTGCCTTACTCTTACTCCATTATCTCATCGAGA	772
Qy	853	TTCAGGATACACTTAAGATCTAGCCGAGCTGAGAACAAAGCCATGAAAGAGCAAGTCTTG	912
Db	773	TTCAGGACACAGTGAAGTACACCACTCAGAAGAGAGCATGAAGAGCAACACTTG	832
Qy	913	TGGAGGTATCAACACGACCTTTTTTCTACATCTTATGTGGATGCATCGGCTATGCTGCAT	972
Db	833	TGAGCGTCAGTGTAA CGACTATGTTCTATGTTCTGTGTGGATGTATGGGATATGCACCT	892
Qy	973	TTGGAACAATGCCCCCTGGAGATTTCCTCACAGATTTTCGGGTTTTTCGAGCCCTTTTGGC	1032
Db	893	TTGAGACTTGTCTCGGGGAAATCTCTTAAACCGGTTTCGGGTTTTTAAATCCTTTATTTGGC	952
Qy	1033	TCATTGACTTTTGCAAACGCTTGCATCGCTGCTCCACCTTATTGGTGGCCCTATCAGAGTGTTG	1092
Db	953	TTCTTTGACATTTGCAATGACGCCATTGTGATTTTCACTTATTGGTGGCATACCAAGTCTATT	1012
Qy	1093	CGCAGCCGATATTCCAGTTTGTGTGAAAAAATTCAAACAGAAAACTATCCAGACAAACAGT	1152
Db	1013	GCCAACTCTGTTTGCTTTTCATCGAAGCAAGCTTCCATTTCAATTCCTCTGATAGTGAGT	1072
Qy	1153	TCATCAGCTTCGAAATATTGATTAAGGTACCTTTTCCTTGGAAAAATTCAACATTAGAGCTCT	1212
Db	1073	TCATTGCAAAAGATATCAAAATTTCCAATTTCTTGGTTTCAAGCCCTCTCGGCTTGAATGCT	1132
Qy	1213	TCAGATTGGTGTGGAGACAGCTTATGTGGTTTATAACCACTGTTGTAGCTATGATATTC	1272
Db	1133	TCAGTTGATATCGAGGACAGTGTTTTGATCATTAACGACAGTTATCTCAATGCTTCTTC	1192
Qy	1273	CTTTCTTCAACCGCATCTTAGGTCTTATCGGAGCAGCTTCTCTTCGGCCTTTTAAACGTTT	1332
Db	1193	CGTTTTTCAACGACGTTGTGGGTCTGCTCGGGCACTAGGGTTTTTGGCCA TTGACGGTGT	1252
Qy	1333	ATTTCCTCTGGAGATGCATTTGCACAAACCAAGATTAAAGAGTACTCTGCTAGATGGA	1392
Db	1253	ATTTTCCAGTGGAAATGTACATCGCGCAAGAAAGATACCTAGATGGAGCACCAGATGGG	1312
Qy	1393	TTGGCTGTAAACCGATGTGCTATGTTTGCTTGATCGTCTCGCTCTTAGCTGACGCCGAT	1452
Db	1313	TTTGGCTTCAAGTCTTCAGCTTAGGGTGTCTAGTAGTTAGCAATGCTGCGAGCTGCAGGGT	1372
Qy	1453	CCATCGCAGGACTTTAAGTAGTGTCAAAACCTACAAGCCCTTCGGGA	1500
Db	1373	CCATAGCTGGAGTACTTCTTGATCTTAAGTCTCTACAAGCCATTTTCGAA	1420

RESULT 4

```

US-09-938-842A-1482
; Sequence 1482, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1482
; LENGTH: 1482

```

Db 1063 CACCCCATCTTTGCTTATTTGAAAATCGTGAGAGATATCCAGCAATGACTTC 1122
Qy 1155 ATCACTTCTGATATTCAGTAAACGTACC---TTTCCCTTGGAAAATTCACATTAGCCTC 1211
Db 1123 CTCAGCAGAGAAATTTAAATCAGAAATCCCGAGTTTAAAGTCTCTTACAAAGTAAACGTT 1182
Qy 1212 TTCAGATGGTGTGAGAGACAGCTTATGTGTTATTAACAAGTGTAGCTATGATATTC 1271
Db 1183 TTCAGATGGTGTGAGAGAGTGTGCTTGTGTACAAACAGCGTATGATGCTGATG 1242
Qy 1272 CCTTCTTCAAGCCGATCTTAAAGTCTTATCGAGAGAGCTTCTTGGCCCTTAAAGGTT 1331
Db 1243 CCGTATTTTAAACAGCGTGTGCGGATCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGGCTT 1302
Qy 1332 TATTTCCCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1391
Db 1303 TATTTCCCGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1362
Qy 1392 ATTGCGCTGAGAAACGATGCTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 1451
Db 1363 GGTGTGTTACAGATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATG 1422
Qy 1452 TCATGCGCAGAGCTTATTAAGTATGCTTAAACCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 1508
Db 1423 TCATGCGCAGAGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 1479

RESULT 5

US-09-770-149-475
Sequence 475, Application US/0970149
Patent No. US2002005963A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Mathew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Woessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Kricke, Waja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hubban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
SOFTWARE: FastSeq for Windows Version 4.0
SEO ID NO 475
LENGTH: 660
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-770-149-475

Query Match 11.4%; Score 191.6; DB 10; Length 660;
Best Local Similarity 61.6%; Pred. No. 2.5e-46;
Matches 324; Conservative 0; Mismatches 199; Indels 3; Gaps 1;
Qy 981 AATGCCCTGAGATTTCTCAGAGATTTGGGTTTTCGAGCCCTTTGGCTCATTTGAC 1040

Db 1 AAGACACCGGAAACCTCTTAAACGGTTTTGTTTCTACAAATCCGTTTGGCTCCTTGAC 60
Qy 1041 TTTCGAAACGCTTGATCGCTGTCACCTTATTTGAGCTATCAGGTGTTGGCGACCG 1100
Db 61 GTGGCTAACGCTGCTATGATATCCATCTTTGAGAGCTTATCAAGTCTTTGGTCAGCCC 120
Qy 1101 ATATTCAGTTTGTGAGAAAAAATGCAACAGAACTATCCAGACAAAGTTCACTACT 1160
Db 121 ATCTGCTTATTTAGAAACAGAGCTGCGCTAGTTTCCGACAGTACCTTGGTACCC 180
Qy 1161 TCTGAATATTCAGTAAAGTACTTCTTGG---AAATTCAACTTACCTTCCAG 1217
Db 181 AAGAAATACGAAATCCGAATCCCTGTTTATGATCCCTTAAAGTCAACGTTTTCAG 240
Qy 1218 TTGATGAGAGACAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1277
Db 241 GCAGTTTACGAAAGCGGTTTGTGTTTGGACACCTGTATCATGCTTATGCGGTTT 300
Qy 1278 TTCAACGCGATCTTAAAGTCTTATCGAGAGAGCTTCTTGGCTTTAAACGTTTATTC 1337
Db 301 TTCAACGAGCGTAGAGATTTAGGTGCGTTAGGTTTGGCTTTGACGCTTACTT 360
Qy 1338 CCTGTGAGATGACATTTGCAACAAACAGATTAAAGATCTGTGATGATGATGATGATGATG 1397
Db 361 CCGTGAAGATGATATTAAGACAGAGAAAGTTGAGAGATGAGATGAGATGAGATGAGATGAG 1420
Qy 1398 CTGAAACAGATGCTATGTTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1457
Db 421 CTGCAATGTTGAGCTGTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1480
Qy 1458 GCAGACTTATTAAGTATGCTTAAACCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 1503
Db 481 GCCGAGTATGCTAGTACCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 526

RESULT 6

US-09-878-574-3976
Sequence 3976, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEO ID NO 3976
LENGTH: 406
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-003-Q1-B1-E11
US-09-878-574-3976

Query Match 10.7%; Score 180; DB 10; Length 406;
Best Local Similarity 65.3%; Pred. No. 4.8e-43;
Matches 264; Conservative 0; Mismatches 140; Indels 0; Gaps 0;
Qy 216 GGCTCCGAGATGTTGCTTAAAGATGGCTATAGCTCAGCTTGTGGATCGGAGGACA 275
Db 2 GGTTCGAGGTCTATCTCTTGATGGCAATTGACAGATGGGTGGAGTGTGCTT 61
Qy 276 TCGATCTTACTATTTTCTGCTCATTTACTTACTTACCTCCACCAATGCTGGCATTCG 335
Db 62 GCAAGTCTTTTCTTCTCTTTGATACATCTTACCTCCACCTCTTCCGTGACTGT 121
Qy 336 TACGTCGCGCGAGTCCGTCACCGGAAAAAGGAATTAACCTTACATGACGTTGTTGCA 395
Db 122 TACGTTCACTGACCTGATCCTGATCATGCAAGCGAACTACACATATTCAGGTTTCAAA 181

QY 396 TCTTACTCGGTGGTAGGAAATGCGAGCTCTGTGGAGTGGCACAATATGGGAATCTGATT 455
Db 182 GCCAACCTTAGGAGGAAGAAAATTTACGTGTGTGGATGGCTCAGTATATAAATCTTGT 241
QY 456 GGGGTCACCTGTTGGTTTACACCACTCACTGCTTCTTATTAGTTTGGTAGCGGTAGGAAATCG 515
Db 242 GGTGTAAACAATCGGCTACACTATAAATGATCACTTATGATGGGGCGGTGAAGAAGTCG 301
QY 516 AACTGCTTCCAGATAAAGGGACACACTCGGATTTGTAATGTAATGTAATGTAATGTAATG 575
Db 302 AACTGTTTACACAACATGCCATCAAGACGAGTGAAGATTTAAGGACAAACGCTTTTATG 361
QY 576 GCGGTTTTTGGTATCATTTCAAGTTATTTTACCCAGATCCCAAA 619
Db 362 ATTGCTTTTGGCTGCATCCAAATTTCTTCCAAACCAATACCAAA 405
RESULT 7
US-09-878-574-2601
; Sequence 2601, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 2601
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-023-Q1-B1-B12
US-09-878-574-2601
Query Match 8.8%; Score 149; DB 10; Length 382;
Best Local Similarity 63.7%; Pred. No. 5.9e-34;
Matches 249; Conservative 0; Mismatches 130; Indels 12; Gaps 1;

QY 546 GATTGTACTATATCGAATTTATCGTATATGCGGTTTTTGGTATCATTTCAAGTTATTTCT 605
Db 4 GAGTGCAAAAGTTAAGGACAAACGCTTTTATGATTTGCTTTTGGCTGCAATCCAAATTTCTTA 63
QY 606 AGCCAGATCCCAAAATTTCCACAGCTCTTTTCTTCCATTATGCGCCAGCTCATGTCC 665
Db 64 AGCCAAATACCAAACTTCCATAGCTCTCTTGGCTCTCTATCGTACGACTGTTATGCT 123
QY 666 TTTACTTATGCAACTATTGGAATTCGGTCTAGCCATCGCAACCGTCTGACGTTGGGAAAGTG 725
Db 124 TTTGCTTATCTTCATTTGGGCTTGGCTTTCCATAGGCAAAATCATAGTTGGGGACAC 183
QY 726 GGTAAAGACAGTATGACGGGACAGCGTTGGAGTAGATGTAAACCGCACTCAAAAGATA 785
Db 184 GTGCGAAACAACTTAAC-----AGGGGTGGAAGTTTCGGGAACGGAAGGTT 231
QY 786 TGGAGATCGTTTTCAGCGGTTGGGNCATAGCTTGGCTATGCTTATGCCAGGTTCTC 845
Db 232 TGGAAATGTTTCAAGCTATCGGTACATTTGGCTTTGCTTTATGCTTTTCTAATGCTTA 291
QY 846 ATCGAGATTGAGATACATAGATCTAGCCAGCTGAGCAACAAAGCCATGAAGAGACA 905
Db 292 ATTGAGATCCAGACACACTGAATCAAGCCCACTGAGAACAAAGTCAATGAGAGACA 351
QY 906 AGTCTTTGGGAGTATCAACACCACCTTTTT 936
Db 352 AGTTTGAATGGCATATGACTACAACTTTG 382

RESULT 8
US-09-878-574-3664
; Sequence 3664, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3664
; LENGTH: 387
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-007-Q1-B1-F10
US-09-878-574-3664

Query Match 8.0%; Score 135.4; DB 10; Length 387;
Best Local Similarity 70.4%; Pred. No. 5.8e-30;
Matches 181; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
QY 135 AAGAACGTGATGAAGATGGTCGAGAGAAGCGTACCGGAGCGTGGCTTACCGCGAGTGGC 194
Db 131 AAAAATTCGACGATGATGGACGAGTCAGAAAGCGGTACATGATAAATCGGAGTGGC 190
QY 195 CATATTATCAGCGCGGTGATAGGCTCCGAGTGTGTCTTTAGCATGGGCTATAGCTCAG 254
Db 191 CATATCATACGCGGATGATAGGCTCAGGAGTGTGTCTTGCATGGGCAATTCACAA 250
QY 255 CTGGTTGGATCGCAGGACATCGATCTTACTCATTTTCTGTTTCATTACTTACTTACC 314
Db 251 ATGGTTGGGTGGCTGGCCCTGCGTCTCTTTGCTTCTTTTCATCCTTACTTACT 310
QY 315 TCCACCATGTTGCGGATTTGCTACCGTGCAGCGGATCCCGTACCGGAAACCGAATTAC 374
Db 311 TCCACTCTTCTTGGCGACTGTTATGTTTCACTGATCTGTTTCATGCGCAAGCAAACTAC 370
QY 375 ACTTACATGGAGTTGT 391
Db 371 ACCTATCCGATGTTGT 387

RESULT 9
US-09-924-035A-35/c
; Sequence 35, Application US/09924035A
; Patent No. US20020142319A1
; GENERAL INFORMATION:
; APPLICANT: Grilach, Jrn
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2011US
; CURRENT APPLICATION NUMBER: US/09/924,035A
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,784
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-924-035A-35

Query Match 7.1%; Score 119.8; DB 10; Length 481;
Best Local Similarity 61.9%; Pred. No. 2.5e-25;
Matches 190; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

OY	1197	TTCAACATTTAGCCCTTCGAATTTGTTGGAGACAGCTTATGTGGTTATTAACACTGTT	1256
Db	446	TACAAAGTCAACGTTTTCAAGACAGTTTACCAAGCGGGTTGTGGTTTTGACCACTGTG	387
OY	1257	GTACGCTATGATATTCCTCTTCCTTCAACGCGATCTTAGCTTTATCGAGCAAGCTTCCTTC	1316
Db	386	ATATTCATGCTTATGCGGTTTTTCAAGACGTCGTAGGGAATTTTAGTGCCTTAGAGTTT	327
OY	1317	TGGCCTTTAAACGGTTTATTTTCCCTGTGGAGATGCACATTGCAACAACCAAGTTAAGAG	1376
Db	326	TGGGCTTTGACGGTTTACTTTCGCGTGGAGATGTATATTAAGACAGAGAAAGTTGAGAGA	267
OY	1377	TACTCTCTAGATGAGATTGGCGCTGGAAAAAGATGCTAGTGTCTTGAATGCTCTCGCTC	1436
Db	266	TGGAGTATGAAGTGGGGTTTCTGTCCAGATGTTGAGCTGTGGTTGTTTGAATGATCAAGTTG	207
OY	1437	TTTACCTCACGCGGATCCATCGCAGGACTTATAGTAGTCAAAAACATACAAAGCCCTTC	1496
Db	206	GTCCCGGAGTTGGCTTCATCGCCGAGTATGCTAGACCTTAAGGTTTTTACAAAGCCGTTTC	147
OY	1497	CGGACTA 1503	
Db	146	AAGACTA 140	

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RESULT 10
US-09-878-574-103
: Sequence 103, Application US/09878574
: Patent No. US20020110548A1
: GENERAL INFORMATION:
: APPLICANT: Byrum, Joseph R.
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Thompson, Michael D.
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
: TITLE OF INVENTION: Plants
: FILE REFERENCE: 38-21(15401)B
: CURRENT APPLICATION NUMBER: US/09/878,574
: CURRENT FILING DATE: 2001-12-21
: PRIOR APPLICATION NUMBER: 09/333,535
: PRIOR FILING DATE: 1999-06-14
: NUMBER OF SEQ ID NOS: 15775
: SEQ ID NO 103
: LENGTH: 383
: TYPE: DNA
: ORGANISM: Glycine max
: OTHER INFORMATION: Clone ID: LIB3028-056-Q1-B1-B2
US-09-878-574-103

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	Query Match	Similarity	6.0%	Score	10.1.4	DB	10	Length	383
	Best Local	Similarity	60.2%	Pred.	No.	5.6e-20			
	Matches	168	Conservative	0	Mismatches	111	Indels	0	Gaps
QY	131	GACAAAGAAAGCTGCATGAAGATGTCGAGAGAAAGCGTACCGGAGCGTGCTTACCGCGAG	190						
Db	87	GTCCAAATTTCTACGATGATGATGTCATCTTAAACCAACAGGGAACGTTTGACCTTCAAG	146						
QY	191	TGCGATATTATACAGGCGCGGTGATAGCTCCGAGAGTGGTCTTTAGCATGGGCTTAC	250						
Db	147	CTCCGACATATTAACAGCAGTGCTGGGTCTTGGGAGTGTCTTTGGCATGGGCCATTGGC	206						
QY	251	TGAGCTGTGGATGCGCAGGACATGCATCTTACTACTTTCTGCTCATTTACTT	310						
Db	207	TCAATGGGTTGGGTGCTGGGCGCTGTATGTATGATCTTTCAGTGTGATACGTTGA	266						
QY	311	CACCTCCACCATGCTTGCCGATTTGCTACACGTCGCGAGTCCGATCCACCGAAAAAGAA	370						
Db	267	TACGAGCTGCTTCTGGCGATTTGTTATGCTGCGCGGTGACCCCGTTACCGGAAAGAA	326						
QY	371	TTACACTTACATGACGCTGTTGCATCTTACTCTGGTG	409						
Db	327	CTATACTTTCATGATGATGCAATTCATCACTTCTTTGGCG	365						

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RESULT 11
US-09-878-574-5991
; Sequence 5991, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Ia Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Placids
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 5991
; LENGTH: 264
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701097612H1
US-09-878-574-5991

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	Query Match	5.6%;	Score 94.4;	DB 10;	Length 264;
	Best Local Similarity	60.5%;	Pred. No. 5.1e-18;		
	Matches 155;	Conservative 0;	Mismatches 101;	Indels 0;	Gaps
Qy	1140	CCAGACACAAAGTTCACTCTTGAAATATTCAGTAAACGTAACCTTTCTCTGGAAATTC	1139		
Db	7	CCATATGTGATATTTTATGACACAGAGATTGAAGTACCAATCCCTGGTTGCAAACTTAC	6		
Qy	1200	AACATTAGCCTCTTCAGATTGTGTGGAGAGACGCTTATGTGTTATATACCACTGTGTA	1258		
Db	67	AAGTCACACCTCTTCAGGTTGGTTGGAGAGACCTTTTGTGATTTTGTCAACTGTGATA	126		
Qy	1260	GCTATGATATTTCCCTTTCTTCACGCGATCTTAGGCTTTATGGGAGCAGTCTCTTCG	1319		
Db	127	GCGATGCTCCACCATCTTTCATATGACATTGTATCCGTTATTTGGAGCCATTGGATTTGG	186		
Qy	1320	CCTTTAAACGGTTATTTTCCCTGTGGAGATGCACATTGCACAAACCAAGATTAAAGATAC	1379		
Db	187	CCCCCTACTGTGATTTATACCAAGTGGAGATGTATATATCACTCAAACTTAGATACAAAGTG	246		
Qy	1380	TCTGTAGATGATGTG	1395		
Db	247	GGCATTAATGGATAG	262		

```

Query Match      5.2%   Score 88.2   DB 10   Length 386,
US-09-878-574-3794
RESULT 12
US-09-878-574-3794
; Sequence 3794, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3794
; LENGTH: 386
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LTB3028-005-Q1-B1-G8
US-09-878-574-3794

```

Best Local Similarity 58.0%; Pred. No. 4.2e-16;
Matches 156; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 111 GCTACACGCTGTCGACCCGACAAAGACGTCGATGAAGATGGTCGAGAGAGCGTACC 170
|||
Db 117 GACAAACCAAGCCCTTATCGAACTGGAACGACGATGATGGCAGATCAAGAAAC 176
|||
QY 171 GGGACGTGCTACGGCGAGTGGCATATATACCGCGGTGATAGGCTCCGGAGTGTG 230
|||
Db 177 GGGATGCTGGAGCTGCTAACATACACATATTAACAGTGGTGTAGGGCGAGGGGTG 236
|||
QY 231 TCTTTAGCATGGCTATAGCTAGCTGCTGTTGATCGCAGGACATCGATCTTACTCAT 290
|||
Db 237 TCTTTGGCATGGTATGCGACAACTAGGATGGTGGATGCGATGACCATATACC 296
|||
QY 291 TTCTGCTTCATTACTTACTTACCTCCACATGCTTGGCGATGTTACCGTGGCGGAT 350
|||
Db 297 TTTTCAGCTGTCGCCATTTTCACTTACAATCTTGTAGCTGATTTTACAGATATCCAG 356
|||
QY 351 CCGGTCACCGGAAGGAAATTACATTA 379
|||
Db 357 CCTGTCACTGGCAAGAAATATACTTA 385
|||

RESULT 13
US-09-878-574-1977
; Sequence 1977, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Thompson, Michael J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-08-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 1977
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-030-Q1-B1-F3
US-09-878-574-1977

Query Match 5.2%; Score 88; DB 10; Length 307;
Best Local Similarity 55.6%; Pred. No. 4.2e-16;
Matches 169; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 374 CACTTACATGGAGTGTGTCGATCTTACCTCGGTGGTAGAAAGTCAGCTCTGTGGAGT 433
|||
Db 1 CTCTTACATGGATGCTGTTAGAGTTTATCTTGGTTATAAAGACATGTTAGCTGGCTT 60
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QY 434 GGCACAAATGGAATCTGATTTGGGGTCACTGTTTGTACCACTACCTCTCTATTAG 493
|||
Db 61 CCTTCAATTTTGGACTTGTATGGTACTAGTATGCTTATGTAACACACAGCAACTAG 120
|||
QY 494 TTTTGTAGCGGTAGGAAATCGAACTGCTTCCACGATAAAGGCGACACTGCGGATGTAC 553
|||
Db 121 TCTGAGTGCATCTGATGATCAATTTGTTATCACAGAAAGGCATGAAGCTCTTTGTA 180
|||
QY 554 TATATCGAATTTCCGTATATGCGGTTTTTGGTATCATTCAGTTATTCTTTAGCCAGAT 613
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Db 181 ATATGTTGGCAATCTGTAATATGCACTGTTTGGACTTTTGCAGTTGTAATGTCATTAT 240
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QY 614 CCGAATTTCCCAAGCTCTCTTTCTTTCCATTTATGGCGGAGTCATGCTCTTTACTTTA 673
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Db 241 ACCGGATCTCCCAATGCAATGGGTTTTCAGTTGTTGAGCACTATGCTCTTTTACATA 900
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QY 674 TGCA 677
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Db 301 CTCA 304

RESULT 14

US-09-923-876-317
; Sequence 317, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 317
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700156744H1
; NAME/KEY: unsure
; LOCATION: 88, 92, 96
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-317

Query Match 4.7%; Score 80; DB 10; Length 238;
Best Local Similarity 61.2%; Pred. No. 8e-14;
Matches 145; Conservative 0; Mismatches 88; Indels 4; Gaps 1;

QY 328 CCGATTGCTACGTCGCGCGGATCCCTCACGCGGAACGGAATACACTTACATGGAGC 387
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Db 1 CCGACTGCTACGCGACGCGGACCCCTCCACGCGAAACGGAACCGCACCTACATGGAGC 60
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QY 388 TTGTTCCGATCTTACCTCGGTGGTAGMAAGTGCAGCT----CTGTGGAGTGGCAATAT 443
|||
Db 61 TCGTCCGCTCATGCTCGGCGCTAGAGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTG 120
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QY 444 GGAATCTGATTTGGGTGCATGTTGTTTACCATCACTGCTTCTATTAGTTTGTAGCG 503
|||
Db 121 GCGATCTCTTGGGGACAATGTTGGGCTACACCATCACCACTGCCACGAGCATCATGCC 180
|||
QY 504 GTAGGAATCGAACTGTTCCACGATAAGGGCACACTGCGGATTTGACTATATCG 560
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Db 181 GTCGCGCGCAGGACTGCGCGCACCAACAGGGGCCACGACGCGGCTCGCGCTCGCTCG 237
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RESULT 15

US-09-878-574-3185
; Sequence 3185, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3185
; LENGTH: 382
; TYPE: DNA

; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-014-Q1-B1-F5
US-09-878-574-3185

Query Match 3.4%; Score 56.8; DB 10; Length 382;
Best Local Similarity 59.1%; Pred. No. 7e-07;
Matches 97; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

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Qy 144 GATGAAGATGTCGAGAGAGCGTACCGGACGTGCTTACGGCGAGTGGCATATTATC 203
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Db 217 GATGATGATGAGACATGCCAAAGGACTGGGAATTGCAAGTGTGTAGCTCATATCATT 276
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Qy 204 ACGGCGGTATAGGCTCCGAGGTGTCTTTAGCATGGGCTATAGCTGAGTTGG 263
    |||||
Db 277 ACTGCTGTATTGTTCTGGGTGTTCTTCTCTGCAAGGAGCACTCCCAATTAGGATGG 336
    |||||
Qy 264 ATGCGAGGAGACATGATCTTACTCATTTCTCGTTCATTACTTA 307
    |||||
Db 337 ATTGAGGGGCAATTTCTTGTGTTGTGCAATTGTCACTTA 380
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Search completed: December 1, 2002, 10:32:14
Job time : 78 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 08:56:52 ; Search time 2037 Seconds
(without alignments)
13396.856 Million cell updates/sec

Title: US-09-854-562-1

Perfect score: 1685
Sequence: 1 CTTAAACACTTTATTTATC.....TTCACAAAAA 1685

Scoring table: IDENTITY NUC
Gapop 10_0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
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24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578.4	34.3	614	10	AV826998 AV826998
2	473.8	28.1	545	9	AI995511 701675547
3	434	25.8	434	10	AV796991 AV796991
4	416.4	24.7	418	10	AV804261 AV804261
5	415	24.6	415	10	AV803440 AV803440
6	411.4	24.4	414	10	AV803032 AV803032

Result No.	Score	Query Match	Length	DB ID	Description
7	409.4	24.3	411	10	AV820846 AV820846
8	407	24.2	407	10	AV815645 AV815645
9	404.8	24.0	421	10	AV810513 AV810513
10	402	23.9	419	10	AV818296 AV818296
11	396	23.5	408	10	AV814816 AV814816
12	394.8	23.4	405	10	AV812283 AV812283
13	391	23.2	391	10	AV802054 AV802054
14	389	23.1	401	10	AV800991 AV800991
15	386.6	22.9	405	10	AV820975 AV820975
16	371.8	22.1	803	12	BG588608 BG588608
17	368.4	21.9	1756	11	AY109232 AY109232
18	333.4	19.8	667	9	AU237594 AU237594
19	312	18.5	3157	17	AB030808 AB030808
20	300.6	17.8	654	10	AM560155 AM560155
21	288	17.1	603	13	BI096983 BI096983
22	287.4	17.1	617	14	BO850879 BO850879
23	282.4	16.8	825	10	BE040834 BE040834
24	273.2	16.2	741	12	BE999727 BE999727
25	272.2	16.2	726	14	BU023358 BU023358
26	267.2	15.9	560	10	AM203255 AM203255
27	265.8	15.8	592	10	AM737124 AM737124
28	265.4	15.8	390	14	Z18061 Z18061
29	264.8	15.7	676	12	BG449584 BG449584
30	260.4	15.5	619	10	AM586710 AM586710
31	259	15.4	718	14	BO165802 BO165802
32	259	15.4	720	17	BH525612 BH525612
33	259	15.4	777	12	BG582749 BG582749
34	258.4	15.3	582	12	BF423871 BF423871
35	252.6	15.0	614	13	BJ277500 BJ277500
36	250.6	14.9	721	14	BQ856263 BQ856263
37	250.4	14.9	701	14	BQ857040 BQ857040
38	250.2	14.8	569	13	BI698982 BI698982
39	250	14.8	551	13	BMS21152 BMS21152
40	247.6	14.7	700	9	AL505065 AL505065
41	246.8	14.6	561	13	BMS26380 BMS26380
42	246.6	14.6	571	10	AV440612 AV440612
43	245.8	14.6	546	14	BQ453973 BQ453973
44	244.2	14.5	686	12	BF634717 BF634717
45	243.8	14.5	692	14	BO762905 BO762905

ALIGNMENTS

RESULT 1
LOCUS AV826998
DEFINITION AV826998 RAFL9 Arabidopsis thaliana cDNA clone RAF109-10-F18 5', mRNA sequence.
ACCESSION AV826998
VERSION AV826998.1 GI:19869058
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE
AUTHORS Seki,M., Naruse,K., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shingawa,A., Muramatsu,M., Hayashizaki,Y. and Shinzaki,K.
TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rcc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI

and XhoI was ligated to modified Lambda FUC-1 vector (Carinci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pluscript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES	Source	Location/Qualifiers
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		/db_xref="taxon:3702"
		/clone="RAFL09-10-F18"
		/clone_lib="RAFL9"
		/dev_stage="plants at various developmental stages from germination to mature seeds"
		/lab_host="DH10B"
		/note="Site_1: BamHI; Site_2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"
BASE COUNT	141 a 145 c 147 g 179 t	2 others
ORIGIN		
Query Match	34.3%	Score 578.4; DB 10; Length 614;
Best Local Similarity	99.5%	Pred. No. 3.1e-117;
Matches	579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
Qy	1	CTTAAACATTTATTTATCTCTCTCTGTTCTCTCTTTCTCTTTCTCTCATCATGA 60
Db	33	CTTAAACATTTATTTATCTCTCTGTTCTCTCTTTCTCTTTCTCTCATCATGA 92
Qy	61	AGAGTTTCAACACAGAAGGACACAACTCCACGGCGGAATCCGGCGATGCCCTACACCG 120
Db	93	AGAGTTTCAACACAGAAGGACACAACTCCACGGCGGAATCCGGCGATGCCCTACACCG 152
Qy	121	TGTCGGACCCGACAAAGAACGTCGATGAAGATGGTCGAGAGAAGCGTACCGGACGTGGC 180
Db	153	TGTCGGACCCGACAAAGAACGTCGATGAAGATGGTCGAGAGAAGCGTACCGGACGTGGC 212
Qy	181	TTACGGCGAGTGGCGATATTATCACGGCGGTGTATAGGCTCCGGAGTGTTGTCTTAGCAT 240
Db	213	TTACGGCGAGTGGCGATATTATCACGGCGGTGTATAGGCTCCGGAGTGTTGTCTTAGCAT 272
Qy	241	GGGCTATAGCTCAGCTTGGTGGATCGCAGGAGACATCGATCTTACTCATTTTCGTTC 300
Db	273	GGGCTATAGCTCAGCTTGGTGGATCGCAGGAGACATCGATCTTACTCATTTTCGTTC 332
Qy	301	TTACTTACTTCACCTCCACCATGCTTGCCGATTGCTACGTCGCGCGGATCCCGTCACCG 360
Db	333	TTACTTACTTCACCTCCACCATGCTTGCCGATTGCTACGTCGCGCGGATCCCGTCACCG 392
Qy	361	GAAGACGGAATTACATTTACATGACGTGTTGTTCGATCTTACTCGTGGGTAGGAAAGTGC 420
Db	393	GAAGACGGAATTACATTTACATGACGTGTTGTTCGATCTTACTCGTGGGTAGGAAAGTGC 452
Qy	421	AGCTCTGTGGAGTCGCACAAATATGGAATCTGATTGGGTCACGTGGTTGTACACCATCA 480
Db	453	AGCTCTGTGGAGTCGCACAAATATGGAATCTGATTGGGTCACGTGGTTGTACACCATCA 512
Qy	481	CTGCTTCTATTAGTTTGGTAGCGGTAGGGAATCGAACTGCTTCCACGATAAGGGCACA 540
Db	513	CTGCTTCTATTAGTTTGGTAGCGGTAGGGAATCGAACTGCTTTCACGATAAGGGCACA 572
Qy	541	CTGCGGATGTGACTATATTCGAATTTATCCGATATAGCGGGTTT 582
Db	573	CTGCGGATGTGACTATATTCGAATTTATCCGATATAGGNGGTTT 614

RESULT 2
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LOCUS AI995511 545 bp linear EST 08-SEP-1999
DEFINITION 701675547 A. thaliana, Columbia Col-0, inflorescence-1 Arabidopsis
thaliana cDNA clone 701675547, mRNA sequence.
ACCESSION AI995511
VERSION AI995511.1 GI:5842496
KEYWORDS EST.

SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS	1 (bases 1 to 545) Chen,J., Momiyama,M., Chan,B., Mooney,M., Carroon,B., Gilliland,D., Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Broska,P., Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D., Tan,R., Rose,M., Warren,B., Ton,B., Kastyur,K., Borillo,C., Carpio,T., Policky,J., Suzuki,S., Argentine,C., Shah,S., Nobriga,A., Murry,L., Turner,C., Krikorian,G., Elder,L. and Hanson,D.
TITLE	Arabidopsis thaliana Gene Expression MicroArray
JOURNAL	Unpublished (1999)
COMMENT	Contact: David Smoller, ph.D. Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc. 4633 World Parkway Circle, St. Louis, MO 63134, USA Tel: 877-577-2733 Fax: 314-427-3324 Email: service@genomesystems.com.
FEATURES	Location/Qualifiers
SOURCE	1..545

FEATURES
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 email: servicegenomesystems.com.
 Location/Qualifiers
 1. 545
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 /cultivar="Columbia Col-0"
 /db_xref="taxon:3702"
 /clone="701675347"
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 /tissue_type="inflorescence"
 /dev_stage="4 - 7 weeks"
 /notes="Vector: pSPORT; Site 1: NotI, Site 2: SalI; cDNA library was derived from untreated inflorescence tissue from Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks. Plants were grown in 1:1:1 peat moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C under constant light, and watered with fertilizer. cDNA synthesis was initiated using a NotI-oligo(dT) primer. Double-stranded cDNA was blunted, ligated to SalI adaptors digested with NotI, size-selected, and cloned into the NotI and SalI sites of the pSPORT vector."
 BASE COUNT 169 a 105 c 110 g 149 t 12 others
 ORIGIN
 Query Match 28.1%; Score 473.8; DB 9; Length 545;
 Best Local Similarity 95.9%; Pred. No. 3.6e-94;
 Matches 512; Conservative 0; Mismatches 18; Indels 4; Gaps 3;
 QY 1119 AAAAAATGCAACGAACATATCC--AGACACAAAGTTTCATCACTTCTGAAATATTCAGTAA 1176
 Db 534 AAAAAATGCAACGAACATATCCAGACACAAAGTNCATCACTTCTGAAATATTCAGTAA 475
 QY 1177 ACGTACCTTTCTTGGAAAAATTCACATAGCTCTTCAGATGGTGGAGACAGCTT 1236
 Db 474 ACGTACCTTTCTTGGAAAAATTCACATAGCTCTTCAGATGGTGGAGACAGCTT 415
 QY 1237 ATGTGGTTATAACCACTGTTGTAGCTATGATATTCCTTTTCTTCAACGGGATCTTAGGTC 1296
 Db 414 ATGTGGTTATAACCACTGTTGTAGCTATGATATTCCTTTTCTTCAACGGGATCTTAGGTC 355
 QY 1297 TTATCGGAGCAGTTCTCTCTGCGCTTTTAAACGGTTTATTTCCCTGTGGAGATGCAATTG 1356
 Db 354 TTATCGGAGCAGTTCTCTCTGCGCTTTTAAACGGTTTATATCCCTGTGGAGATGCAATTG 295
 QY 1357 CACAAACCAAGATTAAGAAGTACTCTGTAGATGGATTCGGCTGAAAAAGATGTGCTATG 1416
 Db 294 CACAAACCAAGATTAAGAAGTACTCTGTAGATGGATTCGGCTGAAAAAGATGTGCTATG 235
 QY 1417 TTTGCTTGATCGTCTCGCTCTTAGCTGACGCGGATCCATCGCAGGACTTTATAAGTAGTG 1476
 Db 234 TTTGCTTGATCGTCTCGCTCTTAGCTGACGCGGATCCATCGCAGGACTTTATAAGTAGTG 175
 QY 1477 TCAAAACCTCAAGCCCTTCCGGACTATGCA-TGAGTGAATT-TGAGATCCTCAAGAGAG 1534

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Db 174 TCAAAACCTACCAAGCCCTCCGACATATGACANNAGTAGTCTGTGAGATCCTCAAGAG 115
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Db 114 TCAAAATATATATAGTAGTATGTTGGTCTTTCTGTATTAACATATCTGTCTAAATCCAAATG 55
Qy 1595 AGAATGCTTTATTTGCTAAACATTCATGAATCTCTGTATCTATCTTCAAT 1648
Db 54 AGAATGCTTTATTTGCTAAACATTCATGAATCTCTGTATCTATCTTCAAT 1

RESULT 3
AV796991/c 434 bp mRNA linear EST 29-MAR-2002
LOCUS AV796991 RAF19 Arabidopsis thaliana cDNA clone RAF109-10-F18 3',
ACCESSION AV796991
VERSION AV796991.1 GI:19830974
KEYWORDS EST,
SOURCE chae cress,
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 434)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
CONTACT: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified lambda FLU-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified Bluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.
FEATURES
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/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAF109-10-F18"
/clone_1ib="RAF19"
/dev_stage="plants at various developmental stages from
germination to mature seeds"
/lab_host="DH10B"
/notes="Site 1: BamHI; Site 2: SalI; subjected to
dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
hr) treatments"
BASE COUNT 141 a 93 c 90 g 110 t
ORIGIN
Query Match 25.8%; Score 434; DB 10; Length 434;
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1177 AGCTACCTTTCTCTGGAAAATTAACATTAGCCTTTCAGATGGTGTGAGACAGCTT 1236
Db 434 AGCTACCTTTCTCTGGAAAATTAACATTAGCCTTTCAGATGGTGTGAGACAGCTT 375
Qy 1237 ATGTGTTATTAACACAGCTGTGATGATATATCCCTTTCTTCAACGCGATCTTAGGTC 1296
Db 374 ATGTGTTATTAACACAGCTGTGATGATATATCCCTTTCTTCAACGCGATCTTAGGTC 315
Qy 1297 TTATCGAGACAGCTTCTTCTGCGCTTAAAGGTTATTTCCCTGTGAGATGCACATTG 1356

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Db 314 TTATCGAGACAGCTTCTTCTGCGCTTAAAGGTTATTTCCCTGTGAGATGCACATTG 255
Qy 1357 CACAAACCAAGATTAAAGAGTACTCTGATGATGATTTGCGGTGAAGATGCTATG 1416
Db 254 CACAAACCAAGATTAAAGAGTACTCTGATGATGATTTGCGGTGAAGATGCTATG 195
Qy 1417 TTGCTGTATGCTCTTCTGCTTATGCTGACGCCGATCCATCGCAGACATTATAGTAGTG 1476
Db 194 TTGCTGTATGCTCTTCTGCTTATGCTGACGCCGATCCATCGCAGACATTATAGTAGTG 135
Qy 1477 TCAAAACCTACCAAGCCCTCCGACATATGACATGATTTGAATCTCTCAAGAGATC 1536
Db 134 TCAAAACCTACCAAGCCCTCCGACATATGACATGATTTGAATCTCTCAAGAGATC 75
Qy 1537 AAAAATATATATAGTAGTATGTTGGTCTTTCTGTAAATCTATCTGTCTAATCCAAATGAG 1596
Db 74 AAAAATATATATAGTAGTATGTTGGTCTTTCTGTAAATCTATCTGTCTAATCCAAATGAG 15
Qy 1597 AATGCTTTATTTGCT 1610
Db 14 AATGCTTTATTTGCT 1

RESULT 4
AV804261/c 418 bp mRNA linear EST 29-MAR-2002
LOCUS AV804261 RAF19 Arabidopsis thaliana cDNA clone RAF109-38-H12 3',
DEFINITION AV804261
VERSION AV804261.1 GI:19838246
KEYWORDS EST,
SOURCE chae cress,
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 418)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
CONTACT: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified lambda FLU-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified Bluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.
FEATURES
source Location/Qualifiers
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/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAF109-38-H12"
/clone_1ib="RAF19"
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germination to mature seeds"
/lab_host="DH10B"
/notes="Site 1: BamHI; Site 2: SalI; subjected to
dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
hr) treatments"
BASE COUNT 140 a 81 c 89 g 108 t
ORIGIN

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Query Match      24.7%; Score 416.4; DB 10; Length 418;
Best Local Similarity 99.8%; Pred. No. 1.7e-81;
Matches 417; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1252 CTGTTGTAGCTATGATATTCCTTTCTTCAACGCGATCTTAGGTCTTATCGGAGCAGCTT 1311
DB 418 CTGTTGTAGCTATGATATTCCTTTCTTCAACGCGATCTTAGGTCTTATCGGAGCAGCTT 359

QY 1312 CCTTCGGGCTTTAAAGCGTTTATTTCCCTGTGGAGATGCACATTCGACAAACCAAGATTA 1371
DB 358 CCTTCGGGCTTTAAAGCGTTTATTTCCCTGTGGAGATGCACATTCGACAAACCAAGATTA 299

QY 1372 AGAAGTACTCTGCTAGATGATGCTGCTGAAACGATGCTATGTTTCTGCTGATGCTCT 1431
DB 298 AGAAGTACTCTGCTAGATGATGCTGCTGAAACGATGCTATGTTTCTGCTGATGCTCT 239

QY 1432 CGCTCTTAGCTGCAGCGGATCCATCGCAGGACTTATAAGTAGTGTCACAAACCTACAAGC 1491
DB 238 CGCTCTTAGCTGCAGCGGATCCATCGCAGGACTTATAAGTAGTGTCACAAACCTACAAGC 179

QY 1492 CCTTCGGGACTATGATGATGAGTTGAGATCCTCAAGAGAGTCAAAATATATATAGTAGT 1551
DB 178 CCTTCGGGACTATGATGATGAGTTGAGATCCTCAAGAGAGTCAAAATATATATAGTAGT 119

QY 1552 AGTTTGGTCTTTCTGTTAAACTATCTGCTGCTCAAAATCCTCAAGAGATGCTTTATTGCTA 1611
DB 118 AGTTTGGTCTTTCTGTTAAACTATCTGCTGCTCAAAATCCTCAAGAGATGCTTTATTGCTA 59

QY 1612 AAACCTTCATGAATCTCTCTGTATCTACATCTTTCAATCTAATACATATGAGCTCTTCC 1669
DB 58 AAACCTTCATGAATCTCTCTGTATCTACATCTTTCAATCTAATACATATGAGCTCTTTC 1
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RESULT 5
AV803440/c      AV803440      415 bp      mRNA      linear      EST 29-MAR-2002
LOCUS      AV803440 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-35-112 3',
DEFINITION      mRNA sequence.
ACCESSION      AV803440
VERSION      AV803440.1 GI:19837425
KEYWORDS      EST.
SOURCE      thale cress.
ORGANISM      Arabidopsis thaliana
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REFERENCE
AUTHORS      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
              1 (bases 1 to 415)
              Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
              Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
              Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
              and Shinozaki,K.
              Large scale analysis of Arabidopsis full-length cDNA (2002b)
              Unpublished (2002)
              Contact: Motoaki Seki
              Plant Functional Genomics Research Group
              RIKEN Genomic Sciences Center
              3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
              Tel: 81-298-36-4359
              Fax: 81-298-36-9060
              Email: mseki@tc.riken.go.jp
```

```
TITLE      Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL      Unpublished (2002)
COMMENT      Contact: Motoaki Seki
              Plant Functional Genomics Research Group
              RIKEN Genomic Sciences Center
              3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
              Tel: 81-298-36-4359
              Fax: 81-298-36-9060
              Email: mseki@tc.riken.go.jp
              An Arabidopsis full-length cDNA library was constructed essentially
              as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
              and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
              al., submitted for publication) digested with BamHI and SalI. This
              clone is in a modified pBluescript vector. Please visit our web
              site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for further
              details.
              Location/Qualifiers
              1..415
              /organism="Arabidopsis thaliana"
              /db_xref="taxon:3702"
              /clone="RAFL09-35-112"
              /clone_lib="RAFL9"
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FEATURES
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/lab_host="DH10B"
/notes="Site 1: BamHI; Site 2: SalI; subjected to
dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
hr) treatments"
BASE COUNT      134 a      90 c      85 g      106 t
ORIGIN
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Query Match      24.6%; Score 415; DB 10; Length 415;
Best Local Similarity 100.0%; Pred. No. 3.5e-81;
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1195 AATTCAACATTAGCTCTTTCAGATTGGTGGAGACAGCTTATGTTTAAACCACTG 1254
DB 415 AATTCAACATTAGCTCTTTCAGATTGGTGGAGACAGCTTATGTTTAAACCACTG 356

QY 1255 TTGTAGCTATGATATTCCTTTCTTCAACGCGATCTTAGGTCTTATCGGAGCAGCTTCT 1314
DB 355 TTGTAGCTATGATATTCCTTTCTTCAACGCGATCTTAGGTCTTATCGGAGCAGCTTCT 296

QY 1315 TCTGCGCTTTAAACGTTTATTTCCCTGTGGAGATGCAATTCGACAAACCAAGATTAAGA 1374
DB 295 TCTGCGCTTTAAACGTTTATTTCCCTGTGGAGATGCAATTCGACAAACCAAGATTAAGA 236

QY 1375 AGTACTCTGTAGATGATGCGCTGAAACGATGCTATGTTTCTGATCGTCTCGC 1434
DB 235 AGTACTCTGTAGATGATGCGCTGAAACGATGCTATGTTTCTGATCGTCTCGC 176

QY 1435 TCTTAGCTGCAGCGGATCCATCGCAGGACTTATAAGTAGTGTCAAAACCTACAAGCCCT 1494
DB 175 TCTTAGCTGCAGCGGATCCATCGCAGGACTTATAAGTAGTGTCAAAACCTACAAGCCCT 116

QY 1495 TCCGACTATGATGATGAGTTTGAGATCCTCAAGAGAGTCAAAATATATATAGTAGT 1554
DB 115 TCCGACTATGATGATGAGTTTGAGATCCTCAAGAGAGTCAAAATATATATAGTAGT 56

QY 1555 TTGGTCTTTCTGTTAAACTATCTGCTGTCTAAATCAATGAGATGCTTTATTGC 1609
DB 55 TTGGTCTTTCTGTTAAACTATCTGCTGTCTAAATCAATGAGATGCTTTATTGC 1
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RESULT 6
AV803032/c      AV803032      414 bp      mRNA      linear      EST 29-MAR-2002
LOCUS      AV803032 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-34-B17 3',
DEFINITION      mRNA sequence.
ACCESSION      AV803032
VERSION      AV803032.1 GI:19837017
KEYWORDS      EST.
SOURCE      thale cress.
ORGANISM      Arabidopsis thaliana
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REFERENCE
AUTHORS      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
              1 (bases 1 to 414)
              Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
              Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
              Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
              and Shinozaki,K.
              Large scale analysis of Arabidopsis full-length cDNA (2002b)
              Unpublished (2002)
              Contact: Motoaki Seki
              Plant Functional Genomics Research Group
              RIKEN Genomic Sciences Center
              3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
              Tel: 81-298-36-4359
              Fax: 81-298-36-9060
              Email: mseki@tc.riken.go.jp
```

```
TITLE      Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL      Unpublished (2002)
COMMENT      Contact: Motoaki Seki
              Plant Functional Genomics Research Group
              RIKEN Genomic Sciences Center
              3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
              Tel: 81-298-36-4359
              Fax: 81-298-36-9060
              Email: mseki@tc.riken.go.jp
              An Arabidopsis full-length cDNA library was constructed essentially
              as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
              and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
              al., submitted for publication) digested with BamHI and SalI. This
              al., submitted for publication) digested with BamHI and SalI. This
```


REFERENCE 1 (bases 1 to 407)
 AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
 TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Motoaki Seki
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 RIKEN Genomic Sciences Center
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FEATURES
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 /organism="Arabidopsis thaliana"
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 /clone="RAFL09-87-G16"
 /clone_lib="RAFL9"
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 /lab_host="DH10B"
 /note="Site 1: BamHI; Site 2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"
 BASE COUNT 134 a 78 c 88 g 107 t
 ORIGIN

Query Match 24.2%; Score 407; DB 10; Length 407;
 Best Local Similarity 100.0%; Pred. No. 2.1e-79; Mismatches 0; Indels 0; Gaps 0;
 Matches 407; Conservative 0;
 QY 1263 ATGATATCCCTTTCTTCAACCGATCTTAGGTCTTATCGGAGCAGCTTCTTCTGGCCT 1322
 DB 407 ATGATATCCCTTTCTTCAACCGATCTTAGGTCTTATCGGAGCAGCTTCTTCTGGCCT 348
 QY 1323 TTAACGGTTATTTCCCTGTGGAGATGCACATTGCACAAACCAAGATTAAAGTACTCT 1382
 DB 347 TTAACGGTTATTTCCCTGTGGAGATGCACATTGCACAAACCAAGATTAAAGTACTCT 288
 QY 1383 GCTAGATGATTCGCTGAAACGATGCTATGTTTGTCTGATCGCTCTTAGCT 1442
 DB 287 GCTAGATGATTCGCTGAAACGATGCTATGTTTGTCTGATCGCTCTTAGCT 228
 QY 1443 GCAGCCGATCCATCGCAGGACTTATAAGTAGTGTCAAAACCTTACAAGCCCTTCCGACT 1502
 DB 227 GCAGCCGATCCATCGCAGGACTTATAAGTAGTGTCAAAACCTTACAAGCCCTTCCGACT 168
 QY 1503 ATGCATGAGTGGTTTGGATCCTCAAGAGAGTCAAAAATATATGATGATGTTGGTCTT 1562
 DB 167 ATGCATGAGTGGTTTGGATCCTCAAGAGAGTCAAAAATATATGATGATGTTGGTCTT 108
 QY 1563 TCTGTTAAACTATCTGGTCTTAAATCCAAATGAGATGCTTTATGCTAAACTTCATCA 1622
 DB 107 TCTGTTAAACTATCTGGTCTTAAATCCAAATGAGATGCTTTATGCTAAACTTCATCA 48
 QY 1623 ATCTCTCTGATCTACATCTTTCAATCTAATACATATGAGCTCTTCC 1669
 DB 47 ATCTCTCTGATCTACATCTTTCAATCTAATACATATGAGCTCTTCC 1

RESULT 9
 AV810513/c 421 bp mRNA linear EST 29-MAR-2002
 LOCUS AV810513 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-64-D24 3',
 DEFINITION

mRNA sequence.
 AV810513 GI:19844498
 VERSION AV810513.1
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 421)
 Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
 TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: mseki@rtc.riken.go.jp
 An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.
 FEATURES
 Location/Qualifiers
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 /clone_lib="RAFL9"
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 /lab_host="DH10B"
 /note="Site 1: BamHI; Site 2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"
 BASE COUNT 143 a 78 c 91 g 109 t
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Query Match 24.0%; Score 404.8; DB 10; Length 421;
 Best Local Similarity 98.3%; Pred. No. 6.2e-79; Mismatches 7; Indels 0; Gaps 0;
 Matches 409; Conservative 0;
 QY 1256 TGTAGCTATGATATCCCTTTCTTCAACCGATCTTAGGTCTTATCGGAGCAGCTTCTT 1315
 DB 418 TTAGCTATGATATCCCTTTCTTCAACCGATCTTAGGTCTTATCGGAGCAGCTTCTT 359
 QY 1316 CTGGCTTTAAACGGTTATTTCCCTGTGGAGATGCACATTGCACAAACCAAGATTAAAGAA 1375
 DB 358 CTGGCTTTAAACGGTTATTTCCCTGTGGAGATGCACATTGCACAAACCAAGATTAAAGAA 299
 QY 1376 GTACTCTGATAGATGGATTGCGCTGAAAACGATGCTATGTTGCTTGTATCGTCTCGCT 1435
 DB 298 GTACTCTGATAGATGGATTGCGCTGAAAACGATGCTATGTTGCTTGTATCGTCTCGCT 239
 QY 1436 CTTAGCTCAGCCGGATCCATCGCAGGACTTATAAGTAGTGTCAAAACCTCAAGCCCTT 1495
 DB 238 CTTAGCTCAGCCGGATCCATCGCAGGACTTATAAGTAGTGTCAAAACCTCAAGCCCTT 179
 QY 1496 CCGGACTATGATGAGTGGATTGAGATCCCTCAAGAGAGTCAAAAATATATGATGATGTT 1555
 DB 178 CCGGACTATGATGAGTGGATTGAGATCCCTCAAGAGAGTCAAAAATATATGATGATGTT 119
 QY 1556 TGGTCTTTCTGTTAACTATCTGGTGTCTAAATCAATGAGATGCTTTATTTGCTTAAAC 1615
 DB 118 TGGTCTTTCTGTTAACTATCTGGTGTCTAAATCAATGAGATGCTTTATTTGCTTAAAC 59

QY 1616 TTCATGAATCTCTCTGATATCTACATCTTTCATCTAATATGATGCTTCCAA 1671
DB 58 TTCATGAATCTCTCTGATATCTACATCTTTCATCTAATATGATGCTTCCAA 3

RESULT 10
AVB18296/c
LOCUS AVB18296 419 bp mRNA linear EST 01-APR-2002
DEFINITION AVB18296 RAF19 Arabidopsis thaliana cDNA clone RAF109-97-J12 3',
mRNA sequence.
ACCESSION AVB18296
VERSION AVB18296.1 GI:19860206
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 419)
REFERENCE Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified lambda PLG-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified Bluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/planet/index_e.html) for further
details.

FEATURES
source Location/Qualifiers
1..419
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/clone_1fb="RAF19"
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germination to mature seeds"
/lab_host="DH10B"
/note="Site 1: BamHI; Site 2: SalI; subjected to
dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
hr) treatments"
BASE COUNT 136 a 89 c 88 g 106 t
ORIGIN

Query Match 23.9%; Score 402; DB 10; Length 419;
Best Local Similarity 99.8%; Pred. No. 2.6e-78;
Matches 413; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1166 ATATTGAGTAACGTAACCTTCTCTGGAAATTCACATTAGCCTTTCAGATTGGTGG 1225
DB 414 ATATTGAGTAACGTAACCTTCTCTGGAAATTCACATTAGCCTTTCAGATTGGTGG 356

QY 1226 GAGGACAGCTTATGTTGTTTAACTGTTAGCTATATATTCCTCTTTCACAGC 1285
DB 355 GAGGACAGCTTATGTTGTTTAACTGTTAGCTATATATTCCTCTTTCACAGC 296

QY 1286 GATCTTAGTCTTATCGAGACGCTTCTGAGCCTTTAAAGGTTATTTCCCTGTGGA 1345
DB 295 GATCTTAGTCTTATCGAGACGCTTCTGAGCCTTTAAAGGTTATTTCCCTGTGGA 236

QY 1346 GATGCAATTGCAAAACCAAGATTAAAGAGTACTGTGCTAGATGATGTCGCTGAAAC 1405
DB 235 GATGCAATTGCAAAACCAAGATTAAAGAGTACTGTGCTAGATGATGTCGCTGAAAC 176

QY 1406 GATGTCATGATGTTGGTGTGATGCTCTCGCTCTTAAGTCGAGCCGAGTCAGAGACT 1465
DB 175 GATGTCATGATGTTGGTGTGATGCTCTCGCTCTTAAGTCGAGCCGAGTCAGAGACT 116

QY 1466 TATTAAGTATGTCAAACCTACAGACCCCTCCGAGCTATGATGATGTTGAGATCC 1525
DB 115 TATTAAGTATGTCAAACCTACAGACCCCTCCGAGCTATGATGATGTTGAGATCC 56

QY 1526 TCAAGAGACTCAAAAATATATGATGATGTTGGTCTTCTGTTAAACTATCTGG 1579
DB 55 TCAAGAGACTCAAAAATATATGATGATGTTGGTCTTCTGTTAAACTATCTGG 2

RESULT 11
AVB14816/c
LOCUS AVB14816 408 bp mRNA linear EST 01-APR-2002
DEFINITION AVB14816 RAF19 Arabidopsis thaliana cDNA clone RAF109-84-F17 3',
mRNA sequence.
ACCESSION AVB14816
VERSION AVB14816.1 GI:19856625
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 408)
REFERENCE Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified lambda PLG-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified Bluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/planet/index_e.html) for further
details.

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source Location/Qualifiers
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/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAF109-84-F17"
/clone_1fb="RAF19"
/dev_stage="plants at various developmental stages from
germination to mature seeds"
/lab_host="DH10B"
/note="Site 1: BamHI; Site 2: SalI; subjected to
dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
hr) treatments"
BASE COUNT 134 a 79 c 88 g 107 t
ORIGIN

Query Match 23.5%; Score 396; DB 10; Length 408;
Best Local Similarity 99.8%; Pred. No. 5.4e-77;
Matches 407; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1263 ATGATATTCCTCTTCTCAACGGATCTTAGGCTTATCGAGACGCTTCTTGGCCT 1322
DB 408 ATGATATTCCTCTTCTCAACGGATCTTAGGCTTATCGAGACGCTTCTTGGCCT 349

QY 1323 TTACGGTTTATTTCCCTGTGAGATGCAATTGCAAAACCAAGATTAAAGAGTACTGT 1382

Db 348 TTAACGGTTTATTTCCCTGTGGAGATGCACATTGCACAAACCAAGATTAAAGATCTCT 289
 QY 1383 GCTAGATGATTCGGCTGAAAACGATGCTATGTTTGGCTTGTATGCTCGCTCTTAGCT 1442
 Db 288 GCTAGATGATTCGGCTGAAAACGATGCTATGTTTGGCTTGTATGCTCGCTCTTAGCT 229
 QY 1443 GCA-GCCGGATCCATCGCAGGACTTATAAGTAGTGTCAAAACCTCAAGCCCTTCGGGAC 1501
 Db 228 GCAGGCCGATCCATCGCAGGACTTATAAGTAGTGTCAAAACCTCAAGCCCTTCGGGAC 169
 QY 1502 TATGCATGATGATTTGAGATCTCAAGAGAGTCAAAAATATATGATAGTTGGTCT 1561
 Db 168 TATGCATGATGATTTGAGATCTCAAGAGAGTCAAAAATATATGATAGTTGGTCT 109
 QY 1562 TTCTGTAAACTATCTGGTGTCTAAATCCATGAGATGCTTTATGCTTAAACTTCATG 1621
 Db 108 TTCTGTAAACTATCTGGTGTCTAAATCCATGAGATGCTTTATGCTTAAACTTCATG 49
 QY 1622 AATCTCTGTATCTACATCTTTCAATCTAAATACATATGAGCTCTTCC 1669
 Db 48 AATCTCTGTATCTACATCTTTCAATCTAAATACATATGAGCTCTTCC 1

RESULT 12
 AV812283/c
 LOCUS AV812283 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-72-K15 3',
 DEFINITION mRNA sequence.

ACCESSION AV812283
 VERSION AV812283.1 GI:19846268
 KEYWORDS EST.

SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 405)
 AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
 Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
 Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
 and Shinozaki, K.

TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: mseki@rtc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially
 as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
 and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
 al., submitted for publication) digested with BamHI and SalI. This
 clone is in a modified pBluescript vector. Please visit our web
 site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
 details.

FEATURES
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 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /clone="RAFL09-72-K15"
 /clone_lib="RAFL9"
 /dev_stage="plants at various developmental stages from
 germination to mature seeds"
 /lab_host="DH10B"
 /note="Site 1: BamHI; Site 2: SalI; subjected to
 dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
 hr) treatments"

BASE COUNT 131 a 78 c 85 g 111 t

Query Match 23.4%; Score 394.8; DB 10; Length 405;

Best Local Similarity 99.5%; Pred. No. 1e-76;
 Matches 396; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1280 CAACCGGATCTTAGTCTTTATCGGAGCAGCTTCTCTTGGCCTTTAAACGGTTTATTTCCC 1339
 Db 405 CAACCGGATCTTAGTCTTTATCGGAGCAGCTTCTCTTGGCCTTTAAACGGTTTATTTCCC 346

QY 1340 TGTGGAGATGCACATTGACAAACCAAGATTAAAGATCTCTAGATGGATTCGCT 1399
 Db 345 TGTGGAGATGCACATTGACAAACCAAGATTAAAGATCTCTAGATGGATTCGCT 286

QY 1400 GAAACCGATGTGCTATGTTTGTCTGATCGTCTTCTAGCTCGAGCGGATCCATCGC 1459
 Db 285 GAAACCGATGTGCTATGTTTGTCTGATCGTCTTCTAGCTCGAGCGGATCCATCGC 226

QY 1460 AGGACTTAAAGTAGTGTCAAAACCTCAAGCCCTTCGGACTATGATGAGTGGTTG 1519
 Db 225 AGGACTTAAAGTAGTGTCAAAACCTCAAGCCCTTCGGACTATGATGAGTGGTTG 166

QY 1520 AGATCCTCAAGAGAGTCAAAATATATGATAGTTGGTCTTCTGTTAACTATCTGG 1579
 Db 165 AGATCCTCAAGAGAGTCAAAATATATGATAGTTGGTCTTCTGTTAACTATCTGG 106

QY 1580 TGTCTAAATCCAATGAGATGCTTTATTTGCTAAACCTTCATGAATCTCTGTATCTACA 1639
 Db 105 TGTCTAAATCCAATGAGATGCTTTATTTGCTAAACCTTCATGAATCTCTGTATCTACA 46

QY 1640 TCTTTCAATCTAAATACATATGAGCTCTTCCAAAAAAA 1677
 Db 45 TCTTTCAATCTAAATACATATGAGCTCTTCCAAATATAA 8

RESULT 13
 AV802054/c

LOCUS AV802054 391 bp mRNA linear EST 29-MAR-2002
 DEFINITION AV802054 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-30-110 3',
 mRNA sequence.

ACCESSION AV802054
 VERSION AV802054.1 GI:19836039
 KEYWORDS EST.

SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 391)
 AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
 Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
 Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
 and Shinozaki, K.

TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: mseki@rtc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially
 as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
 and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
 al., submitted for publication) digested with BamHI and SalI. This
 clone is in a modified pBluescript vector. Please visit our web
 site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
 details.

FEATURES
 Location/Qualifiers
 1..391
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /clone="RAFL09-30-110"
 /clone_lib="RAFL9"
 /dev_stage="plants at various developmental stages from
 germination to mature seeds"

BASE COUNT 131 a 78 c 85 g 111 t

Query Match 23.4%; Score 394.8; DB 10; Length 405;

germination to mature seeds"
/lab host="DH10B"
/note="Site 1: BamHI; Site 2: SalI; subjected to
dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
hr) treatments"
BASE COUNT 125 a 84 c 80 g 102 t
ORIGIN

Query Match 23.2%; Score 391; DB 10; Length 391;
Best Local Similarity 100.0%; Pred. No. 7e-76;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1226 GAGGACAGCTTATGTGTTATTAACACTGTGTAGCTATGATATTCCTTTCTTAACGC 1285
1285 GAGGACAGCTTATGTGTTATTAACACTGTGTAGCTATGATATTCCTTTCTTAACGC 332
1286 GATCTTAGGCTTATGTGAGCAGCTCTCTTCGCTTAAAGCTTATTTCCCTGTGGA 1345
1286 GATCTTAGGCTTATGTGAGCAGCTCTCTTCGCTTAAAGCTTATTTCCCTGTGGA 331
1346 GATGCACTTGTGCAACAACCAAGATTAAGAGTACTGTGATGATGATGCGCTGAAAC 1405
271 GATGCACTTGTGCAACAACCAAGATTAAGAGTACTGTGATGATGATGCGCTGAAAC 212
1406 GATGCTATGTTTGTGCTGATGCTGCTCTTGTAGCTGACGCGGATCCATGCGAGACT 1465
211 GATGCTATGTTTGTGCTGATGCTGCTCTTGTAGCTGACGCGGATCCATGCGAGACT 152
1466 TATTAAGTATGTTTGTGCTGATGCTGCTCTTGTAGCTGACGCGGATCCATGCGAGACT 1525
151 TATTAAGTATGTTTGTGCTGATGCTGCTCTTGTAGCTGACGCGGATCCATGCGAGACT 92
1526 TCAAGAGAGCAAAAATATATATAGTATGTTGGCTTTCTTAACTATCTGTGCTA 1585
91 TCAAGAGAGCAAAAATATATATAGTATGTTGGCTTTCTTAACTATCTGTGCTA 32
1586 AATCCAATGAGAAATGCTTATGCTTAAACT 1616
31 AATCCAATGAGAAATGCTTATGCTTAAACT 1

RESULT 14
AV800991/c 401 bp mRNA linear EST 29-MAR-2002
LOCUS AV800991 RAFL9 Arabidopsis thaliana cDNA clone RAF109-26-F16 3'
DEFINITION mRNA sequence.
ACCESSION AV800991
VERSION AV800991.1 GI:19834976
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 401)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
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RIKEN Genomic Sciences Center
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Tel: 81-298-36-4359
Fax: 81-298-36-9060
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as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FIC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified plusvescript vector. Please visit our web

site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.
FEATURES
source Location/Qualifiers
1..401
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAFL09-26-F16"
/dev_stage="plants at various developmental stages from
germination to mature seeds"
/note="Site 1: BamHI; Site 2: SalI; subjected to
dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
hr) treatments"
BASE COUNT 131 a 78 c 88 g 104 t
ORIGIN

Query Match 23.1%; Score 389; DB 10; Length 401;
Best Local Similarity 99.8%; Pred. No. 1.9e-75;
Matches 400; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1270 TCCCTTTCTTAACGCGATCTTAGGCTTATGAGCAGCTCTCTGCTTTAAAGG 1329
401 TCCCTTTCTTAACGCGATCTTAGGCTTATGAGCAGCTCTCTGCTTTAAAGG 342
1330 TTTATTTCCCTGTGAGATGACATTTGCAACAACCAAGATTAAGAGTACTGTGAT 1389
341 TTTATTTCCCTGTGAGATGACATTTGCAACAACCAAGATTAAGAGTACTGTGAT 282
1390 GGATGCGCTGAAACGATGCTATGTTGCTTGTATGCTGCTCTTAAGCTGACCGG 1449
281 GGATGCGCTGAAACGATGCTATGTTGCTTGTATGCTGCTCTTAAGCTGACCGG 222
1450 GATCCATGCGAGACTTATTAAGTA-GTGTCAAACCTAGAGCCCTCGGACTATGAT 1508
221 GATCCATGCGAGACTTATTAAGTAAGTGTGTAACCAAGCCCTTCGACTATGAT 162
1509 GAGTGAATTTGAGATCTCTCAAGAGTCAAAAATATATATAGTATGTTGCTTGT 1568
161 GAGTGAATTTGAGATCTCTCAAGAGTCAAAAATATATATAGTATGTTGCTTGT 102
1569 AATCATCTGCTGTCTAAATCCATGAGAAATGCTTATGCTTAAACTCATGATCTCT 1628
101 AATCATCTGCTGTCTAAATCCATGAGAAATGCTTATGCTTAAACTCATGATCTCT 42
1629 CTGTATCTACATCTTCAATCTTAATCATATGAGCTCTCC 1669
41 CTGTATCTACATCTTCAATCTTAATCATATGAGCTCTCC 1

RESULT 15
AV820975/c 405 bp mRNA linear EST 01-APR-2002
LOCUS AV820975 RAFL11 Arabidopsis thaliana cDNA clone RAF11-13-F24 3'
DEFINITION mRNA sequence.
ACCESSION AV820975
VERSION AV820975.1 GI:19862988
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 405)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
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3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
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An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and Sali. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

source

Location/Qualifiers

1..405

/organism="Arabidopsis thaliana"

/db_xref="taxon:3702"

/clone="RAF11-13-F24"

/clone_lib="RAF11"

/dev_stages="plants at various developmental stages from

germination to mature seeds"

/lab_host="DH10B"

/note="Site_1: BamHI; Site_2: Sali; subjected to various treatments (dehydration, cold, high salt, ABA, heat and UV). Dark-grown plants"

93 c 82 g 100 t

BASE COUNT

ORIGIN

Query Match 22.9%; Score 386.6; DB 10; Length 405;
Best Local Similarity 98.8%; Pred. No. 6.4e-75;
Matches 400; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1207 GCCTCTTCAGATTGGTGGAGACAGCTTATGTGGTTATAACCACTGTGTAGCTATGA 1266
DB 405 GCCTCTTCAGATTGGTGGAGACAGCTTATGTGGTTATAACCACTGTGTAGCTATGA 346

QY 1267 TATTCCTTTCTTCAACGGGATCTTAGGTCTTATCGGACAGCTTCCTTCTGGCCTTTAA 1326
DB 345 TATTCCTTTCTTCAACGGGATCTTAGGTCTTATCGGACAGCTTCCTTCTGGCCTTTAA 286

QY 1327 CGGTTTATTTCCCTGTGGAGATGCACATTCGACAAACCAAGATTAGAAGTACTCTGCTA 1386
DB 285 CGGTTTATTTCCCTGTGGAGATGCACATTCGACAAACCAAGATTAGAAGTACTCTGCTA 226

QY 1387 GATGGATCGCTGAAACGATGTCTATGTTTGTCTGA-TGCTCTCGCTCTTAGCTGCA 1445
DB 225 GATGGATCGCTGAAACGATGTCTATGTTTGTCTGAAGTCTCTAGCTGCA 166

QY 1446 GCCGATCCATCGCAGACTTATAAGTAGTGTCAAAACCTACAAGCCCTCCGGACTATG 1505
DB 165 GCCGATCCATCGCAGACTTATAAGTAGTGTCAAAACCTACAAGCCCTCCGGACTATG 106

QY 1506 CATGAGTGAATTGAGATCCTCAAGAGAGTCAAAATATATGTAGTAGTTGGTCTTTCT 1565
DB 105 CATGAGTGAATTGAGATCCTCAAGAGAGTCAAAATATATGTAGTAGTTGGTCTTTCT 46

QY 1566 GTTAACTATCTGGTCTTAATCCAATCAGATGCTTTATTGCT 1610
DB 45 GTTAACTATCTGGTCTTAATCCAATCAGATGCTTTATTGCT 1

Search completed: December 1, 2002, 10:30:59

Job time : 2062 secs